

PRINTER RUSH

(PTO ASSISTANCE)

Application : 09/703809

Examiner : Hutson

GAU : 1652

From: CA

Location: IDC FMF FDC

Date: 4-21-05

Tracking #: Q078323

Week Date: 4-21-05

DOC CODE	DOC DATE	MISCELLANEOUS
<input type="checkbox"/> 1449		<input type="checkbox"/> Continuing Data
<input type="checkbox"/> IDS		<input type="checkbox"/> Foreign Priority
<input type="checkbox"/> CLM		<input type="checkbox"/> Document Legibility
<input type="checkbox"/> IIFW		<input type="checkbox"/> Fees
<input type="checkbox"/> SRFW		<input checked="" type="checkbox"/> Other See & List 10/260
<input checked="" type="checkbox"/> DRW	<u>10/30/00</u>	
<input type="checkbox"/> OATH		
<input type="checkbox"/> 312		
<input checked="" type="checkbox"/> SPEC	<u>10/30/00</u>	

[RUSH] MESSAGE: Drawing Fig 3 has faded text at the bottom
 Spec. Drawing also have faded illegible text
 at the bottom of page. Please resolve.
 Thank you.

[XRUSH] RESPONSE:

Corrected entire application submitted

Edward Flores

214-866-0001

INITIALS: PS

NOTE: This form will be included as part of the official USPTO record, with the Response document coded as XRUSH.

REV 10/04

119941-1083

4125

Under the Paperwork Reduction Act of 1995, no persons are required to respond to a collection of information unless it displays a valid OMB control number.

TRANSMITTAL FORM

(to be used for all correspondence after initial filing)

Total Number of Pages in This Submission

167

Application Number	09/703,809
Filing Date	October 30, 2000
First Named Inventor	Jeff DeJong
Art Unit	1653
Examiner Name	K. C. Carlson
Attorney Docket Number	UTDA:1083

ENCLOSURES (Check all that apply)

<input type="checkbox"/> Fee Transmittal Form	<input checked="" type="checkbox"/> Drawing(s)	<input type="checkbox"/> After Allowance Communication to TC
<input type="checkbox"/> Fee Attached	<input type="checkbox"/> Licensing-related Papers	<input type="checkbox"/> Appeal Communication to Board of Appeals and Interferences
<input type="checkbox"/> Amendment/Reply	<input type="checkbox"/> Petition	<input type="checkbox"/> Appeal Communication to TC (Appeal Notice, Brief, Reply Brief)
<input type="checkbox"/> After Final	<input type="checkbox"/> Petition to Convert to a Provisional Application	<input type="checkbox"/> Proprietary Information
<input type="checkbox"/> Affidavits/declaration(s)	<input type="checkbox"/> Power of Attorney, Revocation	<input type="checkbox"/> Status Letter
<input type="checkbox"/> Extension of Time Request	<input type="checkbox"/> Change of Correspondence Address	<input checked="" type="checkbox"/> Other Enclosure(s) (please identify below):
<input type="checkbox"/> Express Abandonment Request	<input type="checkbox"/> Terminal Disclaimer	<input type="checkbox"/> Copy of the 10/30/2000 application;
<input type="checkbox"/> Information Disclosure Statement	<input type="checkbox"/> Request for Refund	<input type="checkbox"/> copy of the 10/30/2000 sequence listing;
<input type="checkbox"/> Certified Copy of Priority Document(s)	<input type="checkbox"/> CD, Number of CD(s) _____	<input type="checkbox"/> Copy of the 6/12/2002 sequence listing;
<input type="checkbox"/> Reply to Missing Parts/ Incomplete Application	<input type="checkbox"/> Landscape Table on CD	
<input type="checkbox"/> <input type="checkbox"/> Reply to Missing Parts under 37 CFR 1.52 or 1.53		
<input type="button" value="Remarks"/>		

SIGNATURE OF APPLICANT, ATTORNEY, OR AGENT

Firm Name	Chalker Flores, LLP		
Signature			
Printed name	Edwin S. Flores		
Date	4/29/05	Reg. No.	38,453

CERTIFICATE OF TRANSMISSION/MAILING

I hereby certify that this correspondence is being facsimile transmitted to the USPTO or deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450 on the date shown below:

Signature			
Typed or printed name			Date

This collection of information is required by 37 CFR 1.5. The information is required to obtain or retain a benefit by the public which is to file (and by the USPTO to process) an application. Confidentiality is governed by 35 U.S.C. 122 and 37 CFR 1.11 and 1.14. This collection is estimated to 2 hours to complete, including gathering, preparing, and submitting the completed application form to the USPTO. Time will vary depending upon the individual case. Any comments on the amount of time you require to complete this form and/or suggestions for reducing this burden, should be sent to the Chief Information Officer, U.S. Patent and Trademark Office, U.S. Department of Commerce, P.O. Box 1450, Alexandria, VA 22313-1450. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. SEND TO: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.

If you need assistance in completing the form, call 1-800-PTO-9199 and select option 2.

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

IN RE APPLICATION: Jeff L. DeJong

)

SERIAL NO.:

)

FILED: Concurrently Herewith

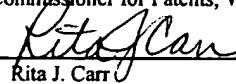
)

FOR: TRANSCRIPTION FACTORS
RELATED TO TFIIA

)

Box Patent Application
Assistant Commissioner
for Patents
Washington, D.C. 20231

"EXPRESS MAILING" Mailing Label No.
EL152179982US. Date of Deposit: June 4, 1999. I
hereby certify that this paper is being deposited with
the U.S. Postal Service Express Mail Post Office to
Addressee Service under 37 CFR 1.10 on the date
shown above and is addressed to the Ass't
Commissioner for Patents, Washington, D.C. 20231.


Rita J. Carr

SEQUENCE LISTING

Dear Sir:

Kindly accept the attached Sequence Listing and disk related to the above-identified
Application for Patent.

Attached please find a hard copy of a Sequence Listing along with a diskette containing a
Sequence Listing in computer readable form in ASCII-DOS format in accordance with the
requirements of 37 C.F.R. 1.824.

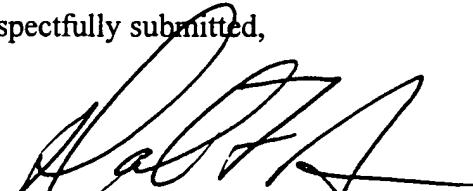
REMARKS

A diskette with a Sequence Listing in ASCII-DOS format is attached and consideration of the application is requested. The content of the paper and computer readable copies are the same as required by 37 C.F.R. 1.821(f).

For the foregoing reasons, the Sequence Listing is submitted to be in order, and complies with the Sequence Rules 37 C.F.R. 1.821 - 1.825.

Dated this 4th day of June, 1999.

Respectfully submitted,



Daniel E. Perez
Attorney for Applicant
Reg. No. 33,755
Gardere & Wynne, L.L.P.
1601 Elm Street, Suite 3000
Dallas, TX 75201
(214) 999-4355 - Tel
(214) 999-4667 - Fax

730212.1

SEQUENCE LISTING

<110> DeJong Dr., Jeff

<120> Transcription Factors Related to TFIIA

<130> 119941-1053

<140>

<141>

<160> 19

<170> PatentIn Ver. 2.0

<210> 1

<211> 1617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (16)..(1449)

<400> 1

gctggaggtg ctgtc atg gcc tgc ctc aac ccg gtg cct aaa ctc tac aga 51

Met Ala Cys Leu Asn Pro Val Pro Lys Leu Tyr Arg

1 5 10

tct gta att gaa gat gta att gaa gga gtt cgg aat cta ttt gct gaa 99

Ser Val Ile Glu Asp Val Ile Glu Gly Val Arg Asn Leu Phe Ala Glu

15 20 25

gaa ggt ata gag gaa caa gtt tta aaa gac ttg aag cag ctc tgg gaa 147

Glu Gly Ile Glu Glu Gln Val Leu Lys Asp Leu Lys Gln Leu Trp Glu

30

35

40

acc aag gtt ttg cag tct aaa gca aca gaa gac ttc ttc aga aat agc 195

Thr Lys Val Leu Gln Ser Lys Ala Thr Glu Asp Phe Phe Arg Asn Ser

45

50

55

60

atc caa tca cct ctg ttt act ctt cag ttg ccg cac agc ttg cac caa 243

Ile Gln Ser Pro Leu Phe Thr Leu Gln Leu Pro His Ser Leu His Gln

65

70

75

aca ttg caa tcg tca aca gca tca tta gtt att cct gct ggt aga act 291

Thr Leu Gln Ser Ser Thr Ala Ser Leu Val Ile Pro Ala Gly Arg Thr

80

85

90

ctt cca agt ttt acc aca gca gaa ctg ggc act tca aac tcc agt gca 339

Leu Pro Ser Phe Thr Thr Ala Glu Leu Gly Thr Ser Asn Ser Ser Ala

95

100

105

aac ttt act ttt cct ggt tat ccc att cat gta cca gca ggt gtg aca 387

Asn Phe Thr Phe Pro Gly Tyr Pro Ile His Val Pro Ala Gly Val Thr

110

115

120

cta cag act gta tct ggt cac ctt tat aaa gtc aat gta cca att atg 435

Leu Gln Thr Val Ser Gly His Leu Tyr Lys Val Asn Val Pro Ile Met

125

130

135

140

gtg aca gag act tct gga aga gca ggt att ctt cag cat cca att cag 483

Val Thr Glu Thr Ser Gly Arg Ala Gly Ile Leu Gln His Pro Ile Gln

145

150

155

caa gta ttt caa cag ctt ggc cag cct tca gta ata caa act agt gtt 531

Gln Val Phe Gln Gln Leu Gly Gln Pro Ser Val Ile Gln Thr Ser Val

160

165

170

c~~a~~ c~~a~~ ttg aat c~~c~~ tgg tct ctt c~~a~~ gca act act gaa aaa t~~c~~ a cag 579
Pro Gln Leu Asn Pro Trp Ser Leu Gln Ala Thr Thr Glu Lys Ser Gln
175 180 185

aga att gaa acc gtg cta cag c~~a~~ ccc gca att c~~t~~ a cct tct ggg c~~c~~ 627
Arg Ile Glu Thr Val Leu Gln Gln Pro Ala Ile Leu Pro Ser Gly Pro
190 195 200

gta gat agg aaa cac t~~t~~ a gaa aat gcc acc agt gat ata ctt gta tct 675
Val Asp Arg Lys His Leu Glu Asn Ala Thr Ser Asp Ile Leu Val Ser
205 210 215 220

cct gga aat gag cat aaa atc gtg cct gaa gct ttg ttg tgt cat cag 723
Pro Gly Asn Glu His Lys Ile Val Pro Glu Ala Leu Leu Cys His Gln
225 230 235

gaa agt tct cac tat atc agt ctt c~~c~~ a ggt gtt gta ttt tct c~~c~~ a cag 771
Glu Ser Ser His Tyr Ile Ser Leu Pro Gly Val Val Phe Ser Pro Gln
240 245 250

gtc tct c~~a~~ aca aat tct gat gtg gag t~~c~~ a gt~~g~~ ctc agt ggt t~~c~~ a gct 819
Val Ser Gln Thr Asn Ser Asp Val Glu Ser Val Leu Ser Gly Ser Ala
255 260 265

agc atg gct c~~a~~ a aat ctg cat gat gag tcc ctc tcc a~~c~~ a agc cct cat 867
Ser Met Ala Gln Asn Leu His Asp Glu Ser Leu Ser Thr Ser Pro His
270 275 280

ggg gct ctc cac cag cac gtg act gat att cag ctt cat att ctt aaa 915
Gly Ala Leu His Gln His Val Thr Asp Ile Gln Leu His Ile Leu Lys
285 290 295 300

aat agg atg tat gga tgt gat tct gta aag c~~a~~ cca aga aat ata gag 963

Asn Arg Met Tyr Gly Cys Asp Ser Val Lys Gln Pro Arg Asn Ile Glu

305

310

315

gaa ccc agc aac ata cct gta tca gag aag gat tct aat tct cag gtg 1011
Glu Pro Ser Asn Ile Pro Val Ser Glu Lys Asp Ser Asn Ser Gln Val

320

325

330

gat tta agc att cgg gtt act gat gat att ggt gaa ata att caa 1059
Asp Leu Ser Ile Arg Val Thr Asp Asp Asp Ile Gly Glu Ile Ile Gln

335

340

345

gta gat gga agc ggt gat aca tct tcc aat gaa gaa ata gga agt aca 1107
Val Asp Gly Ser Gly Asp Thr Ser Ser Asn Glu Glu Ile Gly Ser Thr

350

355

360

aga gat gca gat gag aat gaa ttt cta ggg aat att gac ggg gga gat 1155
Arg Asp Ala Asp Glu Asn Glu Phe Leu Gly Asn Ile Asp Gly Gly Asp
365 370 375 380

ctg aag gta cct gaa gaa gct gac agt att tca aat gag gat tca 1203
Leu Lys Val Pro Glu Glu Ala Asp Ser Ile Ser Asn Glu Asp Ser

385

390

395

gcc aca aac agt agt gat aat gaa gac cct caa gta aac att gta gaa 1251
Ala Thr Asn Ser Ser Asp Asn Glu Asp Pro Gln Val Asn Ile Val Glu

400

405

410

gag gac cct tta aat tct gga gat gat gtt agt gaa cag gat gtg cca 1299
Glu Asp Pro Leu Asn Ser Gly Asp Asp Val Ser Glu Gln Asp Val Pro

415

420

425

gac ctg ttt gac acg gat aat gta att gtc tgt cag tat gat aag att 1347
Asp Leu Phe Asp Thr Asp Asn Val Ile Val Cys Gln Tyr Asp Lys Ile

430

435

440

cat cga agc aag aac aaa tgg aaa ttc tat ttg aaa gat ggt gtt atg 1395
His Arg Ser Lys Asn Lys Trp Lys Phe Tyr Leu Lys Asp Gly Val Met
445 450 455 460

tgt ttt gga ggg aga gac tat gta ttt gca aaa gcc att ggt gat gca 1443
Cys Phe Gly Gly Arg Asp Tyr Val Phe Ala Lys Ala Ile Gly Asp Ala
465 470 475

gag tgg taaaccttgc gagctcagta catctatggt gtgaacatca gttggactat 1499
Glu Trp

attgcattt gtgaattcat ttttatttg aataatgtcc agcacagagc tggcaaatt 1559

ttagttcac tgtatggaat ttaataaaat tataattcag atgcagatac aattacac 1617

<210> 2
<211> 478
<212> PRT
<213> Homo sapiens

<400> 2
Met Ala Cys Leu Asn Pro Val Pro Lys Leu Tyr Arg Ser Val Ile Glu
1 5 10 15

Asp Val Ile Glu Gly Val Arg Asn Leu Phe Ala Glu Glu Gly Ile Glu
20 25 30

Glu Gln Val Leu Lys Asp Leu Lys Gln Leu Trp Glu Thr Lys Val Leu
35 40 45

Gln Ser Lys Ala Thr Glu Asp Phe Phe Arg Asn Ser Ile Gln Ser Pro
50 55 60

Leu Phe Thr Leu Gln Leu Pro His Ser Leu His Gln Thr Leu Gln Ser
65 70 75 80

Ser Thr Ala Ser Leu Val Ile Pro Ala Gly Arg Thr Leu Pro Ser Phe
85 90 95

Thr Thr Ala Glu Leu Gly Thr Ser Asn Ser Ser Ala Asn Phe Thr Phe
100 105 110

Pro Gly Tyr Pro Ile His Val Pro Ala Gly Val Thr Leu Gln Thr Val
115 120 125

Ser Gly His Leu Tyr Lys Val Asn Val Pro Ile Met Val Thr Glu Thr
130 135 140

Ser Gly Arg Ala Gly Ile Leu Gln His Pro Ile Gln Gln Val Phe Gln
145 150 155 160

Gln Leu Gly Gln Pro Ser Val Ile Gln Thr Ser Val Pro Gln Leu Asn
165 170 175

Pro Trp Ser Leu Gln Ala Thr Thr Glu Lys Ser Gln Arg Ile Glu Thr
180 185 190

Val Leu Gln Gln Pro Ala Ile Leu Pro Ser Gly Pro Val Asp Arg Lys
195 200 205

His Leu Glu Asn Ala Thr Ser Asp Ile Leu Val Ser Pro Gly Asn Glu
210 215 220

His Lys Ile Val Pro Glu Ala Leu Leu Cys His Gln Glu Ser Ser His
225 230 235 240

Tyr Ile Ser Leu Pro Gly Val Val Phe Ser Pro Gln Val Ser Gln Thr
245 250 255

Asn Ser Asp Val Glu Ser Val Leu Ser Gly Ser Ala Ser Met Ala Gln
260 265 270

Asn Leu His Asp Glu Ser Leu Ser Thr Ser Pro His Gly Ala Leu His
275 280 285

Gln His Val Thr Asp Ile Gln Leu His Ile Leu Lys Asn Arg Met Tyr
290 295 300

Gly Cys Asp Ser Val Lys Gln Pro Arg Asn Ile Glu Glu Pro Ser Asn
305 310 315 320

Ile Pro Val Ser Glu Lys Asp Ser Asn Ser Gln Val Asp Leu Ser Ile
325 330 335

Arg Val Thr Asp Asp Asp Ile Gly Glu Ile Ile Gln Val Asp Gly Ser
340 345 350

Gly Asp Thr Ser Ser Asn Glu Glu Ile Gly Ser Thr Arg Asp Ala Asp
355 360 365

Glu Asn Glu Phe Leu Gly Asn Ile Asp Gly Gly Asp Leu Lys Val Pro
370 375 380

Glu Glu Glu Ala Asp Ser Ile Ser Asn Glu Asp Ser Ala Thr Asn Ser
385 390 395 400

Ser Asp Asn Glu Asp Pro Gln Val Asn Ile Val Glu Glu Asp Pro Leu
405 410 415

Asn Ser Gly Asp Asp Val Ser Glu Gln Asp Val Pro Asp Leu Phe Asp

420

425

430

Thr Asp Asn Val Ile Val Cys Gln Tyr Asp Lys Ile His Arg Ser Lys

435

440

445

Asn Lys Trp Lys Phe Tyr Leu Lys Asp Gly Val Met Cys Phe Gly Gly

450

455

460

Arg Asp Tyr Val Phe Ala Lys Ala Ile Gly Asp Ala Glu Trp

465

470

475

<210> 3

<211> 3824

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (115)..(3660)

<400> 3

ggactttggg actggacaga cctggtcaca gtctagggtc tacatcttac tggtcgagca 60

acttttagagt caaccttattt gatttcttga caagaccaca atctgatccc aaag atg 117

Met

1

tgc tcc aca aat cca ggc aaa tgg gtc acc ttt gat gat gat cct gct 165

Cys Ser Thr Asn Pro Gly Lys Trp Val Thr Phe Asp Asp Asp Pro Ala

5

10

15

gtt caa tct tct caa aag tca aag aat ttt cct ctg gag aat caa ggt 213

Val Gln Ser Ser Gln Lys Ser Asn Phe Pro Leu Glu Asn Gln Gly

20

25

30

gtc tgt aga cca aat gga ctg aag ctg aac cct cct ggc ctc agg gaa 261
 Val Cys Arg Pro Asn Gly Leu Lys Leu Asn Pro Pro Gly Leu Arg Glu

35

40

45

ttt ccc agt gga tct tcc tcc acc agc agc act cct ctc tcc tcc ccc 309
 Phe Pro Ser Gly Ser Ser Thr Ser Ser Thr Pro Leu Ser Ser Pro
 50 55 60 65

att gta gat ttt tat ttc agt cca gga cct cca agt aac tct cct ctt 357
 Ile Val Asp Phe Tyr Phe Ser Pro Gly Pro Pro Ser Asn Ser Pro Leu

70

75

80

tct aca cct acc aaa gac ttc cca ggt ttt cct ggc atc ccc aaa gca 405
 Ser Thr Pro Thr Lys Asp Phe Pro Gly Phe Pro Gly Ile Pro Lys Ala
 85 90 95

ggg act cat gtg ctt tat cct att cca gaa tca tct tca gac agc cca 453
 Gly Thr His Val Leu Tyr Pro Ile Pro Glu Ser Ser Asp Ser Pro
 100 105 110

ctc gca ata tca gga gga gaa tct tcc tta ctg cct acc aga cca aca 501
 Leu Ala Ile Ser Gly Gly Glu Ser Ser Leu Leu Pro Thr Arg Pro Thr
 115 120 125

tgt tta tcc cat gcc ttg tta ccc agt gac cac tca tgt aca cat cca 549
 Cys Leu Ser His Ala Leu Leu Pro Ser Asp His Ser Cys Thr His Pro
 130 135 140 145

act ccc aaa gta ggt ctt cca gat gaa gtt aat cct caa cag gct gaa 597
 Thr Pro Lys Val Gly Leu Pro Asp Glu Val Asn Pro Gln Gln Ala Glu
 150 155 160

agc cta gga ttc caa agt gat gat ctc ccc cag ttt cag tat ttt cga 645
Ser Leu Gly Phe Gln Ser Asp Asp Leu Pro Gln Phe Gln Tyr Phe Arg
165 170 175

gag gac tgt gct ttt tca agt cca ttt cgg aaa gat gaa ggc agt gat 693
Glu Asp Cys Ala Phe Ser Ser Pro Phe Arg Lys Asp Glu Gly Ser Asp
180 185 190

tcc cat ttc acc ctt gac cca cca gga agc aaa aag atg ttc tca tca 741
Ser His Phe Thr Leu Asp Pro Pro Gly Ser Lys Lys Met Phe Ser Ser
195 200 205

aga aac aag gag atg cct att gac caa aaa agc cta aat aag tgt tca 789
Arg Asn Lys Glu Met Pro Ile Asp Gln Lys Ser Leu Asn Lys Cys Ser
210 215 220 225

ctc aac tat atc tgt gag aag ctt gaa cat ctc cag tca gct gag aac 837
Leu Asn Tyr Ile Cys Glu Lys Leu Glu His Leu Gln Ser Ala Glu Asn
230 235 240

caa gac tca ctt aga agt ttg tct atg cac tgt cta tgt gct gaa gaa 885
Gln Asp Ser Leu Arg Ser Leu Ser Met His Cys Leu Cys Ala Glu Glu
245 250 255

aat gcc tct tcc ttt gtc ccc cac aca ctc ttc agg agt cag cca aaa 933
Asn Ala Ser Ser Phe Val Pro His Thr Leu Phe Arg Ser Gln Pro Lys
260 265 270

tcc gga tgg tct ttc atg ctg aga att cct gag aag aag aat atg atg 981
Ser Gly Trp Ser Phe Met Leu Arg Ile Pro Glu Lys Lys Asn Met Met
275 280 285

tct tcc cgg caa tgg gga cca att ttt ctg aaa gtt ttg cct gga gga 1029
Ser Ser Arg Gln Trp Gly Pro Ile Phe Leu Lys Val Leu Pro Gly Gly

290

295

300

305

att ttg cag atg tat tat gaa cag gga tta gaa aaa cca ttt aaa gag 1077
Ile Leu Gln Met Tyr Tyr Glu Gln Gly Leu Glu Lys Pro Phe Lys Glu

310

315

320

ata cag ctt gat cca tat tgt agg ctt tct gaa ccc aag gtt gag aac 1125
Ile Gln Leu Asp Pro Tyr Cys Arg Leu Ser Glu Pro Lys Val Glu Asn

325

330

335

ttc agt gta gca gga aaa atc cac act gtg aag att gaa cat gtg tct 1173
Phe Ser Val Ala Gly Lys Ile His Thr Val Lys Ile Glu His Val Ser

340

345

350

tac aca gaa aaa agg aaa tac cat tct aag aca gaa gta gtt cat gaa 1221
Tyr Thr Glu Lys Arg Lys Tyr His Ser Lys Thr Glu Val Val His Glu

355

360

365

cct gac ata gag cag atg ctg aag ttg ggg tcc aca tcg tac cat gac 1269
Pro Asp Ile Glu Gln Met Leu Lys Leu Gly Ser Thr Ser Tyr His Asp
370 375 380 385

ttc ctt gac ttt ctg act act gtg gag gag gag ctg atg aag ttg cca 1317
Phe Leu Asp Phe Leu Thr Thr Val Glu Glu Leu Met Lys Leu Pro

390

395

400

gct gtt tca aaa cca aaa aag aac tac gag gag caa gaa att tcc ttg 1365
Ala Val Ser Lys Pro Lys Lys Asn Tyr Glu Glu Gln Glu Ile Ser Leu

405

410

415

gaa att gtg gac aac ttt tgg ggt aaa gtc aca aaa gaa gga aaa ttt 1413
Glu Ile Val Asp Asn Phe Trp Gly Lys Val Thr Lys Glu Gly Lys Phe

420

425

430

gtt gaa agt gct gtg ata actcaa att tat tgc ctc tgc ttt gtg aat 1461
Val Glu Ser Ala Val Ile Thr Gln Ile Tyr Cys Leu Cys Phe Val Asn
435 440 445

ggg aac ctg gaa tgc ttt tta acc ttg aat gac ctt gag ttg ccg aag 1509
Gly Asn Leu Glu Cys Phe Leu Thr Leu Asn Asp Leu Glu Leu Pro Lys
450 455 460 465

cga gat gaa tcc tat tat gag aag gac tca gaa aaa aag ggg att gat 1557
Arg Asp Glu Ser Tyr Tyr Glu Lys Asp Ser Glu Lys Lys Gly Ile Asp
470 475 480

att ctt gac tac cat ttt cat aag tgt gtg aat gta caa gaa ttt gag 1605
Ile Leu Asp Tyr His Phe His Lys Cys Val Asn Val Gln Glu Phe Glu
485 490 495

caa tca aga atc att aag ttt gta cct ctg gat gcc tgc cgg ttt gag 1653
Gln Ser Arg Ile Ile Lys Phe Val Pro Leu Asp Ala Cys Arg Phe Glu
500 505 510

ctg atg cgt ttc aag act ttg tat aat ggg gat aat ctt ccc ttt tcc 1701
Leu Met Arg Phe Lys Thr Leu Tyr Asn Gly Asp Asn Leu Pro Phe Ser
515 520 525

ttg aag tct gta gtg gtt gtc cag gga gca tac gtg gaa ctt cag gct 1749
Leu Lys Ser Val Val Val Val Gln Gly Ala Tyr Val Glu Leu Gln Ala
530 535 540 545

ttt gtc aac atg gcc tca ttg gcg cag agg tca tcc tat gct ggt tcc 1797
Phe Val Asn Met Ala Ser Leu Ala Gln Arg Ser Ser Tyr Ala Gly Ser
550 555 560

tta agg tcc tgt gac aat ata agg ata cac ttt cct gtc cca tcg cag 1845
Leu Arg Ser Cys Asp Asn Ile Arg Ile His Phe Pro Val Pro Ser Gln

565

570

575

tgg atc aag gcc ctt tgg acc atg aac ctc cag agg cag aag tct ctg 1893
Trp Ile Lys Ala Leu Trp Thr Met Asn Leu Gln Arg Gln Lys Ser Leu

580

585

590

aaa gct aaa atg aac cgc cga gca tgt ctg ggg agt tta cag gaa ctt 1941
Lys Ala Lys Met Asn Arg Arg Ala Cys Leu Gly Ser Leu Gln Glu Leu

595

600

605

gaa tct gaa cct gtc att caa gtc act gtg ggg tca gca aaa tat gag 1989
Glu Ser Glu Pro Val Ile Gln Val Thr Val Gly Ser Ala Lys Tyr Glu
610 615 620 625

agt gcc tac cag gca gtg gta tgg aag ata gat cgg ctt cca gac aaa 2037
Ser Ala Tyr Gln Ala Val Val Trp Lys Ile Asp Arg Leu Pro Asp Lys

630

635

640

aat tca agt cta gat cat ccc cat tgt ctg tca tac aaa tta gag ctt 2085
Asn Ser Ser Leu Asp His Pro His Cys Leu Ser Tyr Lys Leu Glu Leu

645

650

655

gga tca gac caa gaa att ccc tct gat tgg tat cca ttt gct act gtt 2133
Gly Ser Asp Gln Glu Ile Pro Ser Asp Trp Tyr Pro Phe Ala Thr Val

660

665

670

cag ttt tcc gtg cct gac acc tgt gcc tca agg aca gag gtc agg tct 2181
Gln Phe Ser Val Pro Asp Thr Cys Ala Ser Arg Thr Glu Val Arg Ser

675

680

685

ctg gga gtg gag agt gat gtc cag cca cag aaa cat gtt cag cag cga 2229
Leu Gly Val Glu Ser Asp Val Gln Pro Gln Lys His Val Gln Gln Arg
690 695 700 705

gct tgc tac aac atc cag cct aaa ctc tac aga tct gta att gaa gat 2277
Ala Cys Tyr Asn Ile Gln Pro Lys Leu Tyr Arg Ser Val Ile Glu Asp
710 715 720

gta att gaa gga gtt cggt aat cta ttt gct gaa gaa ggt ata gag gaa 2325
Val Ile Glu Gly Val Arg Asn Leu Phe Ala Glu Glu Gly Ile Glu Glu
725 730 735

caa gtt tta aaa gac ttg aag cag ctc tgg gaa acc aag gtt ttg cag 2373
Gln Val Leu Lys Asp Leu Lys Gln Leu Trp Glu Thr Lys Val Leu Gln
740 745 750

tct aaa gca aca gaa gac ttc ttc aga aat agc atc caa tca cct ctg 2421
Ser Lys Ala Thr Glu Asp Phe Phe Arg Asn Ser Ile Gln Ser Pro Leu
755 760 765

ttt act ctt cag ttg ccg cac agc ttg cac caa aca ttg caa tcg tca 2469
Phe Thr Leu Gln Leu Pro His Ser Leu His Gln Thr Leu Gln Ser Ser
770 775 780 785

aca gca tca tta gtt att cct gct ggt aga act ctt cca agt ttt acc 2517
Thr Ala Ser Leu Val Ile Pro Ala Gly Arg Thr Leu Pro Ser Phe Thr
790 795 800

aca gca gaa ctg ggc act tca aac tcc agt gca aac ttt act ttt cct 2565
Thr Ala Glu Leu Gly Thr Ser Asn Ser Ala Asn Phe Thr Phe Pro
805 810 815

ggt tat ccc att cat gta cca gca ggt gtg aca cta cag act gta tct 2613
Gly Tyr Pro Ile His Val Pro Ala Gly Val Thr Leu Gln Thr Val Ser
820 825 830

ggt cac ctt tat aaa gtc aat gta cca att atg gtg aca gag act tct 2661
Gly His Leu Tyr Lys Val Asn Val Pro Ile Met Val Thr Glu Thr Ser

835	840	845	
gg a aga gca ggt att ctt cag cat cca att cag caa gta ttt caa cag 2709			
Gly Arg Ala Gly Ile Leu Gln His Pro Ile Gln Gln Val Phe Gln Gln			
850	855	860	865
ctt ggc cag cct tca gta ata caa act agt gtt cca caa ttg aat cca 2757			
Leu Gly Gln Pro Ser Val Ile Gln Thr Ser Val Pro Gln Leu Asn Pro			
870	875	880	
tgg tct ctt caa gca act act gaa aaa tca cag aga att gaa acc gtg 2805			
Trp Ser Leu Gln Ala Thr Thr Glu Lys Ser Gln Arg Ile Glu Thr Val			
885	890	895	
cta cag caa ccc gca att cta cct tct ggg cca gta gat agg aaa cac 2853			
Leu Gln Gln Pro Ala Ile Leu Pro Ser Gly Pro Val Asp Arg Lys His			
900	905	910	
tta gaa aat gcc acc agt gat ata ctt gta tct cct gga aat gag cat 2901			
Leu Glu Asn Ala Thr Ser Asp Ile Leu Val Ser Pro Gly Asn Glu His			
915	920	925	
aaa atc gtg cct gaa gct ttg ttg tgt cat cag gaa agt tct cac tat 2949			
Lys Ile Val Pro Glu Ala Leu Leu Cys His Gln Glu Ser Ser His Tyr			
930	935	940	945
atc agt ctt cca ggt gtt gta ttt tct cca cag gtc tct caa aca aat 2997			
Ile Ser Leu Pro Gly Val Val Phe Ser Pro Gln Val Ser Gln Thr Asn			
950	955	960	
tct gat gtg gag tca gtg ctc agt ggt tca gct agc atg gct caa aat 3045			
Ser Asp Val Glu Ser Val Leu Ser Gly Ser Ala Ser Met Ala Gln Asn			
965	970	975	

ctg cat gat gag tcc ctc tcc aca agc cct cat ggg gct ctc cac cag 3093
Leu His Asp Glu Ser Leu Ser Thr Ser Pro His Gly Ala Leu His Gln
980 985 990

cac gtg act gat att cag ctt cat att ctt aaa aat agg atg tat gga 3141
His Val Thr Asp Ile Gln Leu His Ile Leu Lys Asn Arg Met Tyr Gly
995 1000 1005

tgt gat tct gta aag caa cca aga aat ata gag gaa ccc agc aac ata 3189
Cys Asp Ser Val Lys Gln Pro Arg Asn Ile Glu Glu Pro Ser Asn Ile
1010 1015 1020 1025

cct gta tca gag aag gat tct aat tct cag gtg gat tta agc att cg 3237
Pro Val Ser Glu Lys Asp Ser Asn Ser Gln Val Asp Leu Ser Ile Arg
1030 1035 1040

gtt act gat gat att ggt gaa ata att caa gta gat gga agc ggt 3285
Val Thr Asp Asp Ile Gly Glu Ile Ile Gln Val Asp Gly Ser Gly
1045 1050 1055

gat aca tct tcc aat gaa gaa ata gga agt aca aga gat gca gat gag 3333
Asp Thr Ser Ser Asn Glu Glu Ile Gly Ser Thr Arg Asp Ala Asp Glu
1060 1065 1070

aat gaa ttt cta ggg aat att gac ggg gga gat ctg aag gta cct gaa 3381
Asn Glu Phe Leu Gly Asn Ile Asp Gly Gly Asp Leu Lys Val Pro Glu
1075 1080 1085

gaa gaa gct gac agt att tca aat gag gat tca gcc aca aac agt agt 3429
Glu Glu Ala Asp Ser Ile Ser Asn Glu Asp Ser Ala Thr Asn Ser Ser
1090 1095 1100 1105

gat aat gaa gac cct caa gta aac att gta gaa gag gac cct tta aat 3477
Asp Asn Glu Asp Pro Gln Val Asn Ile Val Glu Glu Asp Pro Leu Asn

1110 1115 1120

tct gga gat gat gtt agt gaa cag gat gtg cca gac ctg ttt gac acg 3525
Ser Gly Asp Asp Val Ser Glu Gln Asp Val Pro Asp Leu Phe Asp Thr

1125 1130 1135

gat aat gta att gtc tgt cag tat gat aag att cat cga agc aag aac 3573
Asp Asn Val Ile Val Cys Gln Tyr Asp Lys Ile His Arg Ser Lys Asn

1140 1145 1150

aaa tgg aaa ttc tat ttg aaa gat ggt gtt atg tgt ttt gga ggg aga 3621
Lys Trp Lys Phe Tyr Leu Lys Asp Gly Val Met Cys Phe Gly Arg

1155 1160 1165

gac tat gta ttt gca aaa gcc att ggt gat gca gag tgg taaaccttgt 3670
Asp Tyr Val Phe Ala Lys Ala Ile Gly Asp Ala Glu Trp

1170 1175 1180

gagctcagta catctatTTT gtgaacatca gttggactat attgcataTTT gtgaattcat 3730

tTTTATTTG aatatAGTCC AGCACAGAGC TGTCAAATT TTGTTCACT TGTATGGAA 3790

ttaataaaat tataattcag atgcagatac aatt 3824

<210> 4

<211> 1182

<212> PRT

<213> Homo sapiens

<400> 4

Met Cys Ser Thr Asn Pro Gly Lys Trp Val Thr Phe Asp Asp Asp Pro

1 5 10 15

Ala Val Gln Ser Ser Gln Lys Ser Lys Asn Phe Pro Leu Glu Asn Gln

20

25

30

Gly Val Cys Arg Pro Asn Gly Leu Lys Leu Asn Pro Pro Gly Leu Arg

35

40

45

Glu Phe Pro Ser Gly Ser Ser Ser Thr Ser Ser Thr Pro Leu Ser Ser

50

55

60

Pro Ile Val Asp Phe Tyr Phe Ser Pro Gly Pro Pro Ser Asn Ser Pro

65

70

75

80

Leu Ser Thr Pro Thr Lys Asp Phe Pro Gly Phe Pro Gly Ile Pro Lys

85

90

95

Ala Gly Thr His Val Leu Tyr Pro Ile Pro Glu Ser Ser Ser Asp Ser

100

105

110

Pro Leu Ala Ile Ser Gly Gly Glu Ser Ser Leu Leu Pro Thr Arg Pro

115

120

125

Thr Cys Leu Ser His Ala Leu Leu Pro Ser Asp His Ser Cys Thr His

130

135

140

Pro Thr Pro Lys Val Gly Leu Pro Asp Glu Val Asn Pro Gln Gln Ala

145

150

155

160

Glu Ser Leu Gly Phe Gln Ser Asp Asp Leu Pro Gln Phe Gln Tyr Phe

165

170

175

Arg Glu Asp Cys Ala Phe Ser Ser Pro Phe Arg Lys Asp Glu Gly Ser

180

185

190

Asp Ser His Phe Thr Leu Asp Pro Pro Gly Ser Lys Lys Met Phe Ser

195	200	205
Ser Arg Asn Lys Glu Met Pro Ile Asp Gln Lys Ser Leu Asn Lys Cys		
210	215	220
Ser Leu Asn Tyr Ile Cys Glu Lys Leu Glu His Leu Gln Ser Ala Glu		
225	230	235
Asn Gln Asp Ser Leu Arg Ser Leu Ser Met His Cys Leu Cys Ala Glu		
245	250	255
Glu Asn Ala Ser Ser Phe Val Pro His Thr Leu Phe Arg Ser Gln Pro		
260	265	270
Lys Ser Gly Trp Ser Phe Met Leu Arg Ile Pro Glu Lys Lys Asn Met		
275	280	285
Met Ser Ser Arg Gln Trp Gly Pro Ile Phe Leu Lys Val Leu Pro Gly		
290	295	300
Gly Ile Leu Gln Met Tyr Tyr Glu Gln Gly Leu Glu Lys Pro Phe Lys		
305	310	315
320		
Glu Ile Gln Leu Asp Pro Tyr Cys Arg Leu Ser Glu Pro Lys Val Glu		
325	330	335
Asn Phe Ser Val Ala Gly Lys Ile His Thr Val Lys Ile Glu His Val		
340	345	350
Ser Tyr Thr Glu Lys Arg Lys Tyr His Ser Lys Thr Glu Val Val His		
355	360	365
Glu Pro Asp Ile Glu Gln Met Leu Lys Leu Gly Ser Thr Ser Tyr His		
370	375	380

Asp Phe Leu Asp Phe Leu Thr Thr Val Glu Glu Glu Leu Met Lys Leu
385 390 395 400

Pro Ala Val Ser Lys Pro Lys Lys Asn Tyr Glu Glu Gln Glu Ile Ser
405 410 415

Leu Glu Ile Val Asp Asn Phe Trp Gly Lys Val Thr Lys Glu Gly Lys
420 425 430

Phe Val Glu Ser Ala Val Ile Thr Gln Ile Tyr Cys Leu Cys Phe Val
435 440 445

Asn Gly Asn Leu Glu Cys Phe Leu Thr Leu Asn Asp Leu Glu Leu Pro
450 455 460

Lys Arg Asp Glu Ser Tyr Tyr Glu Lys Asp Ser Glu Lys Lys Gly Ile
465 470 475 480

Asp Ile Leu Asp Tyr His Phe His Lys Cys Val Asn Val Gln Glu Phe
485 490 495

Glu Gln Ser Arg Ile Ile Lys Phe Val Pro Leu Asp Ala Cys Arg Phe
500 505 510

Glu Leu Met Arg Phe Lys Thr Leu Tyr Asn Gly Asp Asn Leu Pro Phe
515 520 525

Ser Leu Lys Ser Val Val Val Val Gln Gly Ala Tyr Val Glu Leu Gln
530 535 540

Ala Phe Val Asn Met Ala Ser Leu Ala Gln Arg Ser Ser Tyr Ala Gly
545 550 555 560

Ser Leu Arg Ser Cys Asp Asn Ile Arg Ile His Phe Pro Val Pro Ser
565 570 575

Gln Trp Ile Lys Ala Leu Trp Thr Met Asn Leu Gln Arg Gln Lys Ser
580 585 590

Leu Lys Ala Lys Met Asn Arg Arg Ala Cys Leu Gly Ser Leu Gln Glu
595 600 605

Leu Glu Ser Glu Pro Val Ile Gln Val Thr Val Gly Ser Ala Lys Tyr
610 615 620

Glu Ser Ala Tyr Gln Ala Val Val Trp Lys Ile Asp Arg Leu Pro Asp
625 630 635 640

Lys Asn Ser Ser Leu Asp His Pro His Cys Leu Ser Tyr Lys Leu Glu
645 650 655

Leu Gly Ser Asp Gln Glu Ile Pro Ser Asp Trp Tyr Pro Phe Ala Thr
660 665 670

Val Gln Phe Ser Val Pro Asp Thr Cys Ala Ser Arg Thr Glu Val Arg
675 680 685

Ser Leu Gly Val Glu Ser Asp Val Gln Pro Gln Lys His Val Gln Gln
690 695 700

Arg Ala Cys Tyr Asn Ile Gln Pro Lys Leu Tyr Arg Ser Val Ile Glu
705 710 715 720

Asp Val Ile Glu Gly Val Arg Asn Leu Phe Ala Glu Glu Gly Ile Glu
725 730 735

Glu Gln Val Leu Lys Asp Leu Lys Gln Leu Trp Glu Thr Lys Val Leu

740

745

750

Gln Ser Lys Ala Thr Glu Asp Phe Phe Arg Asn Ser Ile Gln Ser Pro

755

760

765

Leu Phe Thr Leu Gln Leu Pro His Ser Leu His Gln Thr Leu Gln Ser

770

775

780

Ser Thr Ala Ser Leu Val Ile Pro Ala Gly Arg Thr Leu Pro Ser Phe

785

790

795

800

Thr Thr Ala Glu Leu Gly Thr Ser Asn Ser Ser Ala Asn Phe Thr Phe

805

810

815

Pro Gly Tyr Pro Ile His Val Pro Ala Gly Val Thr Leu Gln Thr Val

820

825

830

Ser Gly His Leu Tyr Lys Val Asn Val Pro Ile Met Val Thr Glu Thr

835

840

845

Ser Gly Arg Ala Gly Ile Leu Gln His Pro Ile Gln Gln Val Phe Gln

850

855

860

Gln Leu Gly Gln Pro Ser Val Ile Gln Thr Ser Val Pro Gln Leu Asn

865

870

875

880

Pro Trp Ser Leu Gln Ala Thr Thr Glu Lys Ser Gln Arg Ile Glu Thr

885

890

895

Val Leu Gln Gln Pro Ala Ile Leu Pro Ser Gly Pro Val Asp Arg Lys

900

905

910

His Leu Glu Asn Ala Thr Ser Asp Ile Leu Val Ser Pro Gly Asn Glu

915

920

925

His Lys Ile Val Pro Glu Ala Leu Leu Cys His Gln Glu Ser Ser His

930 935 940

Tyr Ile Ser Leu Pro Gly Val Val Phe Ser Pro Gln Val Ser Gln Thr

945 950 955 960

Asn Ser Asp Val Glu Ser Val Leu Ser Gly Ser Ala Ser Met Ala Gln

965 970 975

Asn Leu His Asp Glu Ser Leu Ser Thr Ser Pro His Gly Ala Leu His

980 985 990

Gln His Val Thr Asp Ile Gln Leu His Ile Leu Lys Asn Arg Met Tyr

995 1000 1005

Gly Cys Asp Ser Val Lys Gln Pro Arg Asn Ile Glu Glu Pro Ser Asn

1010 1015 1020

Ile Pro Val Ser Glu Lys Asp Ser Asn Ser Gln Val Asp Leu Ser Ile

1025 1030 1035 1040

Arg Val Thr Asp Asp Asp Ile Gly Glu Ile Ile Gln Val Asp Gly Ser

1045 1050 1055

Gly Asp Thr Ser Ser Asn Glu Glu Ile Gly Ser Thr Arg Asp Ala Asp

1060 1065 1070

Glu Asn Glu Phe Leu Gly Asn Ile Asp Gly Gly Asp Leu Lys Val Pro

1075 1080 1085

Glu Glu Glu Ala Asp Ser Ile Ser Asn Glu Asp Ser Ala Thr Asn Ser

1090 1095 1100

Ser Asp Asn Glu Asp Pro Gln Val Asn Ile Val Glu Glu Asp Pro Leu
105 1110 1115 1120

Asn Ser Gly Asp Asp Val Ser Glu Gln Asp Val Pro Asp Leu Phe Asp
1125 1130 1135

Thr Asp Asn Val Ile Val Cys Gln Tyr Asp Lys Ile His Arg Ser Lys
1140 1145 1150

Asn Lys Trp Lys Phe Tyr Leu Lys Asp Gly Val Met Cys Phe Gly Gly
1155 1160 1165

Arg Asp Tyr Val Phe Ala Lys Ala Ile Gly Asp Ala Glu Trp
1170 1175 1180

<210> 5

<211> 261

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(30)

<223> Variable 3' end for both ALF and SALF

<400> 5

gca ttc cca aga agg aca tcg ttt aac acc taaaactcatt taacaaagga 50

Ala Phe Pro Arg Arg Thr Ser Phe Asn Thr

1 5 10

tccgagaaga acagggacag tgtggaaaga aatcttcttg tgatggcata ttgccttc 110

atatttcttc tggaatcatg ttcgcttggc ttcctgatta aaaacacagt ttatggctc 170

tctgcactgc caaaccaata aatttacaga agagaaagct gtattccact gtaccccttg 230

Cagcatcaat aaaactgaca gccaaaaaaaa a

261

<210> 6

<211> 10

<212> PRT

<213> Homo sapiens

<400> 6

Ala Phe Pro Arg Arg Thr Ser Phe Asn Thr

1

5

10

<210> 7

<211> 18

<212> DNA

<213> Homo sapiens

<400> 7

agaaaattcccc tctgatttg

18

<210> 8

<211> 18

<212> DNA

<213> Homo sapiens

<400> 8

agtaaccgcga atgcttaa

18

<210> 9
<211> 18
<212> DNA
<213> Homo sapiens

<400> 9
atgctagctg aaccactg 18

<210> 10
<211> 27
<212> DNA
<213> Homo sapiens

<400> 10
ccatcctaat acgactcact ataggc 27

<210> 11
<211> 23
<212> DNA
<213> Homo sapiens

<400> 11
actcaactata gggctcgagc ggc 23

<210> 12
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 12
ccagaaggta gaattgcggg ttgctgttagc 30

<210> 13
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 13
ggtgctgtca tggcctgcct caacccgg 28

<210> 14
<211> 52
<212> DNA
<213> Homo sapiens

<400> 14
actactata tggcacacca tcaccatcac catgtaccta aactctacag at 52

<210> 15
<211> 30
<212> DNA
<213> Homo sapiens

<400> 15
agttagtggat ccttaccact ctgcattcacc 30

<210> 16
<211> 8
<212> PRT
<213> Homo sapiens

<400> 16
Met His His His His His His Val
1 5

<210> 17
<211> 6
<212> PRT
<213> Homo sapiens

<400> 17
Met Ala Cys Leu Asn Pro
1 5

<210> 18
<211> 23
<212> DNA
<213> Homo sapiens

<400> 18
tactgctcga gcaacttttag agt

23

<210> 19
<211> 29
<212> DNA
<213> Homo sapiens

<400> 19

ggagtttcaa gtgcccaagg ctgctgtgg

29

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Jeff L. DeJong
Serial Number: 09/703,809
Filing Date: October 30, 2000
Group Art Unit: 1653
Examiner: Carlson, Karen C.
Title: TRANSCRIPTION FACTORS RELATED TO TFIIA

Technology Center 1600
Reception Area, 7th Floor
Karen C. Carlson: Sequence Information
Crystal Mall One
1911 South Clark Street
Arlington, VA 22202

RESPONSE TO NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS
CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Dear Sir:

Applicants hereby respectfully submit this Response to the Examiner's Office Action, dated May 23, 2002, due for reply by June 23, 2002. Applicants respectfully request consideration and entry of the following Substitute Sequence Listing. Attached, please find a hard copy of a Substitute Sequence Listing. A substitute computer readable form (CRF) copy of the Substitute Sequence Listing in ASCII-DOS format is provided in accordance with the requirements of 37 C.F.R. 1.825(d).

RESPONSE

Kindly accept and insert in the Specification, a paper copy of the Substitute Sequence Listing as required under 37 C.F.R. 1.821(c) and 1.825(a) and a diskette containing the substitute computer readable form (CRF) copy of the Substitute Sequence Listing in ASCII-DOS format in accordance with the requirements of 37 C.F.R. 1.825(d). Please cancel all previous filed paper copies of the Sequence Listing and replace those with the Substitute Sequence Listing as provided, herewith. The data contained on the substitute paper copy and the substitute CRF includes no new matter. In accordance with 37 C.F.R.

1.825(a), information contained in the Substitute Sequence Listing finds support in the original application, as filed.

REMARKS

Applicants have submitted a Substitute Sequence Listing in response to the Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures and the CRF Problem Report dated May 23, 2002. The Applicants respectfully request entry of the Substitute Sequence Listing.

A diskette containing the substitute CRF copy of the Substitute Sequence Listing in ASCII-DOS format in accordance with the requirements of 37 C.F.R. 1.825(d) is attached and consideration of the Application is requested. The content of the Substitute Sequence Listing and the substitute CRF copy are the same as required by 37 CFR 1.825(b). No new matter is incorporated in the Specification by this Response.

For the foregoing reasons, the Substitute Sequence Listing is submitted to be in order and complies with the Sequence Rules C.F.R. 1.821–1.825.

Dated: June 12, 2002.

Respectfully submitted,

GARDERE WYNNE SEWELL LLP



Edwin S. Flores
Registration No. 38,453
ATTORNEYS FOR APPLICANTS

3000 Thanksgiving Tower
1601 Elm Street
Dallas, Texas 75201-4761
(214) 999-4559 - Telephone
(214) 999-3559 - Facsimile

DALLAS 1153495v1

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- 7. Other: the specification and the claims do not have sequence identification numbers at each sequence as required by 37 CFR 1,821(d).

Applicant Must Provide:

- An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

SEQUENCE LISTING

<110> DeJong, Jeff L.
<120> Transcription Factors Related to TFIIA
<130> 119941-1083
<140> 09/703,809
<141> 2000-10-30
<150> 09/326,529
<151> 1999-06-04
<160> 18
<170> PatentIn version 3.1
<210> 1
<211> 1617
<212> DNA
<213> Homo sapien
<400> 1
gctggagggtg ctgtcatggc ctgcctcaac ccgggtgccta aactctacag atctgttaatt 60
gaagatgtaa ttgaaggagt tcggaatcta tttgctgaag aaggtataaga ggaacaagtt 120
ttaaaaagact tgaagcagct ctggaaacc aagggtttgc agtctaaagc aacagaagac 180
ttcttcagaa atagcatcca atcacctctg tttactcttc agttgccgca cagcttgcac 240
caaacattgc aatcgtaaac agcatcatta gttattcctg ctggtagaaac tcttccaagt 300
tttaccacag cagaactggg cacttcaaacc tccagtgcaa actttacttt tcctggttat 360
cccattcatg taccagcagg tgtgacacta cagactgtat ctggtcacct ttataaagtc 420
aatgtaccaa ttatggtgac agagacttct ggaagagcag gtattctca gcatccaatt 480
cagcaagtat ttcaacagct tggccagcct tcagtaatac aaactagtgt tccacaattg 540
aatccatggc ctctcaagc aactactgaa aaatcacaga gaattgaaac cgtgctacag 600
caacccgcaa ttctacccctc tggccagta gataggaaac acttagaaaa tgccaccagt 660
gatatacttg tatctcctgg aaatgagcat aaaatcgatc ctgaagctt gttgtgtcat 720
cagggaaagtt ctcactatat cagtcttcca ggtgttgtat tttctccaca ggtctctcaa 780
acaaattctg atgtggagtc agtgctcagt gggtcagta gcatggctca aaatctgcat 840
gatgagtcggc tctccacaag ccctcatggg gctctccacc agcacgtgac tgatattcag 900
cttcatattc taaaaatag gatgtatgga tgtgattctg taaagcaacc aagaaatata 960
gaggaaccca gcaacatacc tgcgtcaggag aaggattcta attctcagggt ggatttaagc 1020

attcgggtta ctgatgatga tattggtaaa ataattcaag tagatggaa cggtgataca	1080
tcttccaaatg aagaaatagg aagtacaaga gatgcagatg agaatgaatt tcttaggaaat	1140
attgacgggg gagatctgaa ggtacctgaa gaagaagctg acagtatttc aaatgaggat	1200
tcagccacaa acagtagtgta taatgaagac cctcaagtaa acattgtaga agaggaccct	1260
ttaaattctg gagatgatgt tagtgaacag gatgtgccag acctgtttga cacggataat	1320
gtaattgtct gtcagttatgtaa taagattcat cgaagcaaga acaaattggaa attctatttg	1380
aaagatggtg ttatgtgttt tggagggaga gactatgtat ttgcaaaagc cattggtgat	1440
gcagagtggt aaaccttgtg agctcagttac atctatttg tgaacatcag ttggactata	1500
ttgcataatttgc tgaatttcattttttaatatagtccat gcacagagct gttcaaaattt	1560
tttagttcact gtatggaaattttaataaaaatttataattcaga tgccatgatcata attacac	1617

<210> 2
<211> 478
<212> PRT
<213> Homo sapien

<400> 2

```

Met Ala Cys Leu Asn Pro Val Pro Lys Leu Tyr Arg Ser Val Ile Glu
   1           5           10          15

```

Asp Val Ile Glu Gly Val Arg Asn Leu Phe Ala Glu Glu Gly Ile Glu
20 25 30

Glu Gln Val Leu Lys Asp Leu Lys Gln Leu Trp Glu Thr Lys Val Leu
35 40 45

Gln Ser Lys Ala Thr Glu Asp Phe Phe Arg Asn Ser Ile Gln Ser Pro
50 55 60

Leu Phe Thr Leu Gln Leu Pro His Ser Leu His Gln Thr Leu Gln Ser
65 70 75 80

Ser Thr Ala Ser Leu Val Ile Pro Ala Gly Arg Thr Leu Pro Ser Phe
85 90 95

Thr Thr Ala Glu Leu Gly Thr Ser Asn Ser Ser Ala Asn Phe Thr Phe
 100 105 110

Pro Gly Tyr Pro Ile His Val Pro Ala Gly Val Thr Leu Gln Thr Val
115 120 125

Ser Gly His Leu Tyr Lys Val Asn Val Pro Ile Met Val Thr Glu Thr
130 135 140

Ser Gly Arg Ala Gly Ile Leu Gln His Pro Ile Gln Gln Val Phe Gln
145 150 155 160

Gln Leu Gly Gln Pro Ser Val Ile Gln Thr Ser Val Pro Gln Leu Asn
165 170 175

Pro Trp Ser Leu Gln Ala Thr Thr Glu Lys Ser Gln Arg Ile Glu Thr
180 185 190

Val Leu Gln Gln Pro Ala Ile Leu Pro Ser Gly Pro Val Asp Arg Lys
195 200 205

His Leu Glu Asn Ala Thr Ser Asp Ile Leu Val Ser Pro Gly Asn Glu
210 215 220

His Lys Ile Val Pro Glu Ala Leu Leu Cys His Gln Glu Ser Ser His
225 230 235 240

Tyr Ile Ser Leu Pro Gly Val Val Phe Ser Pro Gln Val Ser Gln Thr
245 250 255

Asn Ser Asp Val Glu Ser Val Leu Ser Gly Ser Ala Ser Met Ala Gln
260 265 270

Asn Leu His Asp Glu Ser Leu Ser Thr Ser Pro His Gly Ala Leu His
275 280 285

Gln His Val Thr Asp Ile Gln Leu His Ile Leu Lys Asn Arg Met Tyr
290 295 300

Gly Cys Asp Ser Val Lys Gln Pro Arg Asn Ile Glu Glu Pro Ser Asn
305 310 315 320

Ile Pro Val Ser Glu Lys Asp Ser Asn Ser Gln Val Asp Leu Ser Ile
325 330 335

Arg Val Thr Asp Asp Asp Ile Gly Glu Ile Thr Gln Val Asp Gly Ser

340

345

350

Gly Asp Thr Ser Ser Asn Glu Glu Ile Gly Ser Thr Arg Asp Ala Asp
355 360 365

Glu Asn Glu Phe Leu Gly Asn Ile Asp Gly Gly Asp Leu Lys Val Pro
370 375 380

Glu Glu Glu Ala Asp Ser Ile Ser Asn Glu Asp Ser Ala Thr Asn Ser
385 390 395 400

Ser Asp Asn Glu Asp Pro Gln Val Asn Ile Val Glu Glu Asp Pro Leu
405 410 415

Asn Ser Gly Asp Asp Val Ser Glu Gln Asp Val Pro Asp Leu Phe Asp
420 425 430

Thr Asp Asn Val Ile Val Cys Gln Tyr Asp Lys Ile His Arg Ser Lys
435 440 445

Asn Lys Trp Lys Phe Tyr Leu Lys Asp Gly Val Met Cys Phe Gly Gly
450 455 460

Arg Asp Tyr Val Phe Ala Lys Ala Ile Gly Asp Ala Glu Trp
465 470 475

<210> 3

<211> 3824

<212> DNA

<213> Homo sapien

<400> 3

ggactttggg actggacaga cctggtcaca gtctagggtc tacatcttac tggtcgagca 60
acttttagagt caacctattt gatttcttga caagaccaca atctgatccc aaagatgtgc 120
tccacaaaatc caggcaaattg ggtcaccttt gatgatgatc ctgctgttca atcttctcaa 180
aagtcaaaga attttccctct ggagaatcaa ggtgtctgta gaccaaattgg actgaagctg 240
aaccctccctg gcctcaggga atttcccagt ggatcttcct ccaccagcag cactcctctc 300
tcctccccca ttgttagattt ttatttcagt ccaggacctc caagtaactc tccttttct 360
acacccatcca aagacttccc aggtttcct ggcattccca aagcaggacatc tcatgtgctt 420
tatcctattc cagaatcatc ttcagacagc ccactcgcaa tatcaggagg agaatcttcc 480

ttactgccta ccagaccaac atgttatcc catgccttgt tacccagtga ccactcatgt 540
acacatccaa ctcccaaagt aggtcttcca gatgaagtta atcctaaca ggctgaaagc 600
ctaggattcc aaagtgtatga tctccccag tttcagtatt ttcgagagga ctgtgtttt 660
tcaagtccat ttccggaaaga tgaaggcagt gattcccatt tcacccttga cccaccagga 720
agcaaaaaga tggtctcatc aagaaacaag gagatgccta ttgaccaaaa aagcctaaat 780
aagtgttcac tcaactatact ctgtgagaag cttgaacatc tccagtcagc tgagaaccaa 840
gactcactta gaagttgtc tatgcactgt ctatgtctg aagaaaaatgc ctctccctt 900
gtccccaca cactcttcag gagtcagcca aaatccggat ggtctttcat gctgagaatt 960
cctgagaaga agaatatgat gtcttcccgg caatggggac caattttct gaaagtttg 1020
cctggaggaa ttttgcagat gtattatgaa cagggattag aaaaaccatt taaagagata 1080
cagcttgcata catattgttag gctttctgaa cccaaagggtt agaacttcag tgttagcagga 1140
aaaatccaca ctgtgaagat tgaacatgtg tcttacacag aaaaaaggaa ataccattct 1200
aagacagaag tagttcatga acctgacata gagcagatgc tgaagttggg gtccacatcg 1260
taccatgact tccttgactt tctgactact gtggaggagg agctgtatgaa gttgccagct 1320
gtttcaaaac caaaaaagaa ctacgaggag caagaaattt cttggaaat tgtggacaac 1380
ttttgggta aagtcacaaa agaaggaaaa tttgtgaaa gtgtgtgat aactcaaatt 1440
tattgcctct gctttgtgaa tggAACCTG gaatgtttt taaccttga tgaccttgag 1500
ttgccgaagc gagatgaatc ctattatgag aaggactcag aaaaaaaggg gattgatatt 1560
cttgactacc atttcataa gtgtgtgaat gtacaagaat ttgagcaatc aagaatcatt 1620
aagttgtac ctctggatgc ctgccggttt gagctgatgc gttcaagac tttgtataat 1680
ggggataatc ttccctttc cttgaagtct gtagtggtt tccagggagc atacgtggaa 1740
cttcaggctt ttgtcaacat ggccctcattt gcgcagaggt catcctatgc tggttccctt 1800
aggcctgtg acaatataag gatacactt cctgtcccat cgcaatggat caagccctt 1860
tggaccatga acctccagag gcagaagtct ctgaaagcta aaatgaaccg ccgagcatgt 1920
ctggggagtt tacaggaact tgaatctgaa cctgtcattt aagtcactgt ggggtcagca 1980
aaatatgaga gtgcctacca ggcagtggtt tggaaagatag atcggcttcc agacaaaaat 2040
tcaagtcttag atcatccccca ttgtctgtca tacaattttt agcttgatc agaccaagaa 2100
attccctctg attggatcc atttgctact gttcagttt ccgtgcctga cacctgtgcc 2160
tcaaggacag aggtcaggtc tctggagtg gagagtgtatg tccagccaca gaaacatgtt 2220

cagcagcgag cttgctacaa catccagcct aaactctaca gatctgtaat tgaagatgt	2280
attgaaggag ttccggaatct atttgctgaa gaaggatata aggaacaagt tttaaaagac	2340
ttgaagcagc tctggaaac caagggtttg cagtc当地caag caacagaaga cttcttcaga	2400
aatagcatcc aatcacctct gtttactctt cagttgccgc acagcttgca ccaaaccattg	2460
caatcgtaa cagcatcatt agttattcct gctggtagaa ctcttccaag ttttaccaca	2520
gcagaactgg gcacttcaaa ctccagtgca aactttactt ttcctggta tcccattcat	2580
gtaccagcag gtgtgacact acagactgtt tctggtcacc tttataaagt caatgtacca	2640
attatggta cagagacttc tgaagagca ggtattcttc agcatccaa tcagcaagta	2700
tttcaacagc ttggccagcc ttcaagtaata caaacttagtg ttccacaatt gaatccatgg	2760
tctcttcaag caactactga aaaatcacag agaattgaaa ccgtgctaca gcaacccgca	2820
attctacctt ctggccagt agataggaaa cacttagaaa atgccaccag tgatatactt	2880
gtatctcctg gaaatgagca taatcgta cctgaagctt tggtgtgtca tcaggaaagt	2940
tctcaactata tcagtcttcc aggtgttgta tttctccac aggtctctca aacaaattct	3000
gatgtggagt cagtgctcag tggtttagt agcatggctc aaaatctgca tgatgagtcc	3060
ctctccacaa gccctcatgg ggctctccac cagcacgtga ctgatattca gttcatatt	3120
cttaaaaata ggatgtatgg atgtgattct gtaaagcaac caagaaatat agaggaaccc	3180
agcaacatac ctgtatcaga gaaggattct aattctcagg tggatttaag cattcgggtt	3240
actgatgatg atattggta aataattcaa gtagatggaa gcgggtatac atcttccaaat	3300
gaagaatag gaagtacaag agatgcagat gagaatgaat ttctagggaa tattgacggg	3360
ggagatctga aggtacctga agaagaagct gacagtattt caaatgagga ttccagccaca	3420
aacagtagtg ataatgaaga ccctcaagta aacattgttag aagaggaccc tttaaattct	3480
ggagatgatg ttagtgaaca ggatgtgcca gacctgtttg acacggataa tgtaattgtc	3540
tgtcagtatg ataagattca tcgaagcaag aacaaatgga aattcttattt gaaagatgg	3600
gttatgtgtt ttggaggag agactatgta tttgcaaaag ccattggta tgccagatgg	3660
taaaccttgt gagctcagta catctatttt gtgaacatca gttggactat attgcataatt	3720
gtgaattcat ttttattttg aatatagtcc agcacagagc tgtaaaattttttagttcac	3780
tgtatggat ttaataaaat tataattcag atgcagatac aatt	3824

<211> 1181
<212> PRT
<213> Homo sapien

<400> 4

Met Cys Ser Thr Asn Pro Gly Lys Trp Val Thr Phe Asp Asp Asp Pro
1 5 10 15

Ala Val Gln Ser Ser Gln Lys Ser Lys Asn Phe Pro Leu Glu Asn Gln
20 25 30

Gly Val Cys Arg Pro Asn Gly Leu Lys Leu Asn Pro Pro Gly Leu Arg
35 40 45

Glu Phe Pro Ser Gly Ser Ser Thr Ser Ser Thr Pro Leu Ser Ser
50 55 60

Pro Ile Val Asp Phe Tyr Phe Ser Pro Gly Pro Pro Ser Asn Ser Pro
65 70 75 80

Leu Ser Thr Pro Thr Lys Asp Phe Pro Gly Phe Pro Gly Ile Pro Lys
85 90 95

Ala Gly Thr His Val Leu Tyr Pro Ile Pro Glu Ser Ser Ser Asp Ser
100 105 110

Pro Leu Ala Ile Ser Gly Gly Glu Ser Ser Leu Leu Pro Thr Arg Pro
115 120 125

Thr Cys Leu Ser His Ala Leu Leu Pro Ser Asp His Ser Cys Thr His
130 135 140

Pro Thr Pro Lys Val Gly Leu Pro Asp Glu Val Asn Pro Gln Gln Ala
145 150 155 160

Glu Ser Leu Gly Phe Gln Ser Asp Asp Leu Pro Gln Phe Gln Tyr Phe
165 170 175

Arg Glu Asp Cys Ala Phe Ser Ser Pro Phe Arg Lys Asp Glu Gly Ser
180 185 190

Asp Ser His Phe Thr Leu Asp Pro Pro Gly Ser Lys Lys Met Phe Ser
195 200 205

Ser Arg Asn Lys Glu Met Pro Ile Asp Gln Lys Ser Leu Asn Lys Cys
210 215 220

Ser Leu Asn Tyr Ile Cys Glu Lys Leu Glu His Leu Gln Ser Ala Glu
225 230 235 240

Asn Gln Asp Ser Leu Arg Ser Leu Ser Met His Cys Leu Cys Ala Glu
245 250 255

Glu Asn Ala Ser Ser Phe Val Pro His Thr Leu Phe Arg Ser Gln Pro
260 265 270

Lys Ser Gly Trp Ser Phe Met Leu Arg Ile Pro Glu Lys Lys Asn Met
275 280 285

Met Ser Ser Arg Gln Trp Gly Pro Ile Phe Leu Lys Val Leu Pro Gly
290 295 300

Gly Ile Leu Gln Met Tyr Tyr Glu Gln Gly Leu Glu Lys Pro Phe Lys
305 310 315 320

Glu Ile Gln Leu Asp Pro Tyr Cys Arg Leu Ser Glu Pro Lys Val Glu
325 330 335

Asn Phe Ser Val Ala Gly Lys Ile His Thr Val Lys Ile Glu His Val
340 345 350

Ser Tyr Thr Glu Lys Arg Lys His Ser Lys Thr Glu Val Val His Glu
355 360 365

Pro Asp Ile Glu Gln Met Leu Lys Leu Gly Ser Thr Ser Tyr His Asp
370 375 380

Phe Leu Asp Phe Leu Thr Thr Val Glu Glu Leu Met Lys Leu Pro
385 390 395 400

Ala Val Ser Lys Pro Lys Lys Asn Tyr Glu Glu Gln Glu Ile Ser Leu
405 410 415

Glu Ile Val Asp Asn Phe Trp Gly Lys Val Thr Lys Glu Gly Lys Phe
420 425 430

Val Glu Ser Ala Val Ile Thr Gln Ile Tyr Cys Leu Cys Phe Val Asn
435 440 445

Gly Asn Leu Glu Cys Phe Leu Thr Leu Asn Asp Leu Glu Leu Pro Lys
450 455 460

Arg Asp Glu Ser Tyr Tyr Glu Lys Asp Ser Glu Lys Lys Gly Ile Asp
465 470 475 480

Ile Leu Asp Tyr His Phe His Lys Cys Val Asn Val Gln Glu Phe Glu
485 490 495

Gln Ser Arg Ile Ile Lys Phe Val Pro Leu Asp Ala Cys Arg Phe Glu
500 505 510

Leu Met Arg Phe Lys Thr Leu Tyr Asn Gly Asp Asn Leu Pro Phe Ser
515 520 525

Leu Lys Ser Val Val Val Gln Gly Ala Tyr Val Glu Leu Gln Ala
530 535 540

Phe Val Asn Met Ala Ser Leu Ala Gln Arg Ser Ser Tyr Ala Gly Ser
545 550 555 560

Leu Arg Ser Cys Asp Asn Ile Arg Ile His Phe Pro Val Pro Ser Gln
565 570 575

Trp Ile Lys Ala Leu Trp Thr Met Asn Leu Gln Arg Gln Lys Ser Leu
580 585 590

Lys Ala Lys Met Asn Arg Arg Ala Cys Leu Gly Ser Leu Gln Glu Leu
595 600 605

Glu Ser Glu Pro Val Ile Gln Val Thr Val Gly Ser Ala Lys Tyr Glu
610 615 620

Ser Ala Tyr Gln Ala Val Val Trp Lys Ile Asp Arg Leu Pro Asp Lys
625 630 635 640

Asn Ser Ser Leu Asp His Pro His Cys Leu Ser Tyr Lys Leu Glu Leu
645 650 655

Gly Ser Asp Gln Glu Ile Pro Ser Asp Trp Tyr Pro Phe Ala Thr Val

660 665 670

Gln Phe Ser Val Pro Asp Thr Cys Ala Ser Arg Thr Glu Val Arg Ser
675 680 685

Leu Gly Val Glu Ser Asp Val Gln Pro Gln Lys His Val Gln Gln Arg
690 695 700

Ala Cys Tyr Asn Ile Gln Pro Lys Leu Tyr Arg Ser Val Ile Glu Asp
705 710 720

Asp Val Ile Glu Gly Val Arg Asn Leu Phe Ala Glu Glu Gly Ile Glu
725 730 735

Gln Val Leu Lys Asp Leu Lys Gln Leu Trp Glu Thr Lys Val Leu Gln
740 745 750

Ser Lys Ala Thr Glu Asp Phe Phe Arg Asn Ser Ile Gln Ser Pro Leu
755 760 765

Phe Thr Leu Gln Leu Pro His Ser Leu His Gln Thr Leu Gln Ser Ser
770 775 780

Thr Ala Ser Leu Val Ile Pro Ala Gly Arg Thr Leu Pro Ser Phe Thr
785 790 795 800

Thr Ala Glu Leu Gly Thr Ser Asn Ser Ser Ala Asn Phe Thr Phe Pro
805 810 815

Gly Tyr Pro Ile His Val Pro Ala Gly Val Thr Leu Gln Thr Val Ser
820 825 830

Gly His Leu Tyr Lys Val Asn Val Pro Ile Met Val Thr Glu Thr Ser
835 840 845

Gly Arg Ala Gly Ile Leu Gln His Pro Ile Gln Gln Val Phe Gln Gln
850 855 860

Leu Gly Gln Pro Ser Val Ile Gln Thr Ser Val Pro Gln Leu Asn Pro
865 870 875 880

Trp Ser Leu Gln Ala Thr Thr Glu Lys Ser Gln Arg Ile Glu Thr Val
885 890 895

Leu Gln Gln Pro Ala Ile Leu Pro Ser Gly Pro Val Asp Arg Lys His
900 905 910

Leu Glu Asn Ala Thr Ser Asp Ile Leu Val Ser Pro Gly Asn Glu His
915 920 925

Lys Ile Val Pro Glu Ala Leu Leu Cys His Gln Glu Ser Ser His Tyr
930 935 940

Ile Ser Leu Pro Gly Val Val Phe Ser Pro Gln Val Ser Gln Thr Asn
945 950 955 960

Ser Asp Val Glu Ser Val Leu Ser Gly Ser Ala Ser Met Ala Gln Asn
965 970 975

Leu His Asp Glu Ser Leu Ser Thr Ser Pro His Gly Ala Leu His Gln
980 985 990

His Val Thr Asp Ile Gln Leu His Ile Leu Lys Asn Arg Met Tyr Gly
995 1000 1005

Cys Asp Ser Val Lys Gln Pro Arg Asn Ile Glu Glu Pro Ser Asn
1010 1015 1020

Ile Pro Val Ser Glu Lys Asp Ser Asn Ser Gln Val Asp Leu Ser
1025 1030 1035

Ile Arg Val Thr Asp Asp Asp Ile Gly Glu Ile Ile Gln Val Asp
1040 1045 1050

Gly Ser Gly Asp Thr Ser Ser Asn Glu Glu Ile Gly Ser Thr Arg
1055 1060 1065

Asp Ala Asp Glu Asn Glu Phe Leu Gly Asn Ile Asp Gly Gly Asp
1070 1075 1080

Leu Lys Val Pro Glu Glu Glu Ala Asp Ser Ile Ser Asn Glu Asp
1085 1090 1095

Ser Ala Thr Asn Ser Ser Asp Asn Glu Asp Pro Gln Val Asn Ile
1100 1105 1110

Val Glu Glu Asp Pro Leu Asn Ser Gly Asp Asp Val Ser Glu Gln
1115 1120 1125

Asp Val Pro Asp Leu Phe Asp Thr Asp Asn Val Ile Val Cys Gln
1130 1135 1140

Tyr Asp Lys Ile His Arg Ser Lys Asn Lys Trp Lys Phe Tyr Leu
1145 1150 1155

Lys Asp Gly Val Met Cys Phe Gly Gly Arg Asp Tyr Val Phe Ala
1160 1165 1170

Lys Ala Ile Gly Asp Ala Glu Trp
1175 1180

<210> 5
<211> 253
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> (1)..(30)
<223>

<400> 5
gca ttc cca aga agg aca tcg ttt aac acc taaaactcatt taacaaagga 50
Ala Phe Pro Arg Arg Thr Ser Phe Asn Thr
1 5 10

tccgagaaga acagggacag tgtggaaaga aatcttcttg tgatggcata tttgcttcct 110
atatttcttc tggaatcatg ttgcgttggc ttccctgatta aaaacacagt tttattgctc 170
tctgcactgc caaaccaata aatttacaga agagaaagct gtattccact gtaccccttg 230
cagcatcaat aaaactgaca gcc 253

<210> 6
<211> 10
<212> PRT
<213> Homo sapien

<400> 6
Ala Phe Pro Arg Arg Thr Ser Phe Asn Thr
1 5 10

<210> 7

<211> 10
<212> PRT
<213> Homo sapien

<400> 7

Ala Phe Pro Arg Arg Thr Ser Phe Asn Thr
1 5 10

<210> 8
<211> 18
<212> DNA
<213> Homo sapien

<400> 8
agaaattccc tctgattg 18

<210> 9
<211> 18
<212> DNA
<213> Homo sapien

<400> 9
agtaacccga atgcttaa 18

<210> 10
<211> 18
<212> DNA
<213> Homo sapien

<400> 10
atgcttagctg aaccactg 18

<210> 11
<211> 29
<212> DNA
<213> Homo sapien

<400> 11
ggagttgaa gtgcccgagg ctgctgtgg 29

<210> 12
<211> 30
<212> DNA
<213> Homo sapien

<400> 12
ccagaaggta gaattgcggg ttgctgtgc 30

<210> 13
<211> 28

<212> DNA
<213> Homo sapien

<400> 13
ggtgctgtca tggcctgcct caaccgg

28

<210> 14
<211> 54
<212> DNA
<213> Homo sapien

<400> 14
actactcata tggcacacca tcaccatcac catgtaccta aactctacag atct

54

<210> 15
<211> 30
<212> DNA
<213> Homo sapien

<400> 15
agtagtggat ctttaccact ctgcatcacc

30

<210> 16
<211> 24
<212> PRT
<213> Homo sapien

<400> 16

Met Glu Thr His Ile Ser His Ile Ser His Ile Ser His Ile Ser His
1 5 10 15

Ile Ser His Ile Ser Val Ala Leu
20

<210> 17
<211> 6
<212> PRT
<213> Homo sapien

<400> 17

Met Ala Cys Leu Asn Pro
1 5

<210> 18
<211> 23
<212> DNA
<213> Homo sapien

<400> 18

tactgctcga gcaactttag agt

23

GGACTTTGGGACTGGACAGACCTGGTCACAGTCAAGTCTAGGTTCTACATCTTACTGGTCGAGCAACTTAGACTAACCTATT
 GATTTCCTGACAAGACCAATCTGATCCAAAGATGTGCTCCACAAATCCAGGCAAATGGTCACCTTGATGATGATC
 CTGCTGTTCAATCTTCTCAAAGTCAAGAATTTCCTGAGAATCAAGGTGCTGAGCAAATGGACTGAAGCTG
 AACCCCTCGGCCTCAGGAAATTCCAGTGGATCTCCTCCACCCAGCAGCACTCCCTCTCCCTCCCCCATTGTAGATT
 TTATTCAGTCCAGGACCTCAAGTAACTCTCTTCTACACCTACAAAGACTTCCAGGTTTCTGGCATCCCCA
 AAGCAGGAGACTATGTGCTTATCCATTCAGAATCATCTCAGACAGCCCACTCGCAATATCAGGAGAGAATCTCC
 TTACTGCTTACAGACCAACATGTTATCCCAGCTGCTTACCGTACGACTCATGTACACATCAACTCCAAAGT
 AGGTCTTCCAGATGAAGTTAATCCTCAACAGGCTGAAAGCCTAGGATTCAAAGTGTGATCTCCAGTTCTAGTATT
 TTGAGAGGAGCTGTGCTTTCAAGTCCATTGAGAAAGATGAAGGAGCTGATTCCACCTTACCCAGGTTGAGGAGA
 AGCAAAAAGATGTTCTCATCAAGAAACAAGGAGATGCCTATTGACCAAAAAAGCTAAATAAGTGTACTCAACTATAT
 CTGAGAGGAGCTGAGACATCTCAGTCAAGGAGAACAGACTACTAGAGTGTGAGTTGCTATGCTATGTGCTG
 AAGAAAATGCCCTCTTCTGCCCCACACTCTCAGGACTGAGCAAATCCGGATGGTCTTCTGAGAATT
 CCTTGAGAAGAAGAATATGATGTTCCCGCAATGGGAGCAATTTCAGGACTGAGGAAATTGCTGAGAAGTGTGAGAATT
 GTATTATGAACAGGGATTAGAAAACCATTAAAGAGATAACGCTTGTGATCATAATTGTAGGTTCTGAGAAGGTTG
 AGAACTTCAGTGTAGCAGGAAAATCCACACTGTGAAGATTGAACTGTGTTACACAGAAAAAGGAAATACATTCT
 AAGACAGAAGTAGTTCATGAACTGACATAGAGCAGATGCTGAAGTTGGGTCACATGTCACATGACTCCCTGACTT
 TCTGACTACTGTGGAGGAGGAGCTGATGAGTTGCTCAGCTGTTCAAACCAAAAAAGAACTACGAGGAGCAAGAAATT
 CCTTGAGAATGTGGACAACCTTGGGTAAGTCAACAAAGAAGGAAATTGTTGAAAGTGTGATAACTCAAATT
 TATTGCTCTGCTTGTGATGAGGAAACTGGAAATGCTGTTAACTTGAATGCTGTTGAGTGGCAGAGATGAATC
 CTATTATGAGAAGGACTCAGAAAAGGGGATGTGATATTCTGACTACATTCTCATAGTGTGAAATGTCACAGAAT
 TTGAGCAATAGAATCTTAAAGTTGATCCTCTGAGCTGCTGAGGAGCTGAGGAGCTGAGGTTCAAGACTTTGTATAAT
 GGGGATAATCTCCCTTCTGAGGACTGCTGAGTGTGAGGAGCTGAGGAGCTACGTGAACTCAGGCTTGTCAACAT
 GCCCTCATGGCGCAGAGGTCATCTATGCTGTTCTTAAGGCTCTGTGACAATATAAGGATAACACTTCTGCCCCAT
 CGCAGTGGATCAAGGCCCTTGGACCATGAACTCCAGAGGAGAAGTCTGTGAAAGCTAAATGAACGCCGAGCATGT
 CTGGGAGTTACAGGAACCTGAATGTCATTCAAGTCAGTCACTGTGGGTCAGCAAATATGAGAGTGCCTACCA
 GGCAGTGGATGGAAGATAGATCGGCTCCAGACAAAATCAACTGAGATCATCCCATGGTCTGTCATACAAATTAG
 AGCTTGGATCAGACCAAGAAAATCCCTCTGATTGGTATCCATTGCTACTGTCAGTTCAGGCTGCTGACACCTGTGCC
 TCAAGGAGAGGTCTGGAGAGTGGAGTGGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGG
 CATCAGCCTAAACTCTACAGATCTGTAATTGAGATGTAATTGAGGAGTGGCAATCTATTGTCAGGAGTATAAGTCAATGTACCA
 AGGAACAAGTTAAAAGACTTGAAGCAGCTCTGGGAAACCAAGGTTTGAGCTAAAGCACAGAAGACTTCTCAGA
 ATAGCATCCAATCACCTCTGTTACTCTCAGTTGCGCAGCAGCTGCACAAACATTGCAATCGTCAACAGCATCATT
 AGTTATTCTGCTGTTAGAACTCTTCAAGTTTACACAGCAGAATGGGACTCTCAAACCTCAGTGCACACTTTACTT
 TTCTGTTATCCATTCTGAGGAGCTGAGGAGCTACAGACTGTCATCTGTCACCTTATAAGTCAATGTACCA
 ATTATGAGGAGGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGG
 TTCAGTAACTACAAACTAGTGTCCACAAATTGAGATCATCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGG
 CCGTGTACAGAACCCGAATTCTACCTCTGGGCACTAGATAGGAAACACTGAGGAGCTGAGGAGCTGAGGAGCTGAGG
 GTATCTCTGAGAATGAGCATAAAATCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGG
 AGGTGTTGATTTCTCCACAGGCTCTCAAACAAATTCTGATGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGG
 AAAATCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGG
 CTAAATCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGG
 GAAGGATTCTAATTCTCAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGG
 GCGGTGTACATCTTCAATTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGG
 GGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGG
 CCCTCAAGTAAACATTGAGAAGAGGACCTTAAATTCTGGAGATGTTAGTGAACAGGAGTGTGAGGAGCTGAGGAGCTGAGG
 ACACGGATAATGTAATTGTCAGTGTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGG
 GTTATGTGTTGGAGGGAGAGACTATGATTGCAAAAGCCATTGGTGTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGG
 CATCTATTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGG
 GTTCAAAATTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGG
 PAVSKPKKNYEISLEIVDNFWGKVTEKGKFVESAVITQIYCLCFCVNGNLECFTLNDLLELPKRDESYEKDSEKKGI
 DILDYHFHKCVNQFEQESRIKVFPLDACRFEMLRFTLYNDNLPSLKSVVVVGAYVELQAFVNMASLAQRSSYAG
 SLRSCDNIRIHFVPSQWIKALWTMNLQRQKSLSAKMNRRACLGSLOQELESEPVQIQTGVSAYESAYQAVVWKIDRLPD
 KNSSLDPHCHLSYKLELGSDQEIPSDWYPFATVQFSVPDTCSARTEVRSLGVESDVQPQKHVQQRACYNIQPKLYRSVIE
 DVIEGVRNLFAEEGIEEQVLKDLKQLWETKVLQLSKATEDFFRNSIQSPLFTLQLPHSLHQTLQSTSASLVIAPGRTPSF
 TTAEGLTSNNSANFTFPGYPIHVPAGVTQTVSGHLYKVNVPIMVTETSGRAGILQHPIQQVFQQLGQPSVIQTSVPQLN
 PWSLQATTEKSQRIETVLLQQPAILPSGPVDRKHLENATSDILVSPGNEHKIVPEALLCHQESSHYISLPGVVFSPQVSQT
 NSDVEVLSGSASMAQNLHDESLSTSPHGALHQHVTDIQLHILKNRMYGCDSVKQPRNIEEPSNIPESEKDSNSQVDLSI
 RVTDDDIGEIIVQDGSGDTSSNEEIGSTRADADENEFLGNIDGGDLKVPEEEADSISNEDSATNSSDNEDPQVNIVEEDPL
 NSGDDVSEQDVPDFDTDNIVCQYDKIHRSKNKWKFYLDGVCMFGGRDYVFAKAIGDAEW

Figure 3.

MCSTNPWKWVTFDDDPAVQSSQKSKNFPLENQGVCRPNGLKLNPPLREFSGSSSTSSTPLSSPIVDFYFSPGPPSNSP
 LSTPTKDFPGFPGPPIKAGTHVLYPIPESSSDSPLAISGGESSLLPRTPTCLSHALLPSDHSCHTPTPKVGLPDEVNPQQA
 ESLGFQSDDLQFOYFREDCAFSSPFRKDEGSDSHFTLDPPGSKKMFSRNKEMPIDQKSLSNCKSLNYICEKLEHLQSAE
 NQDSLRSLSMHCALCAEENASSVPHTLFRSQPKSGWSEMLRIPKEKKNMSSRQWGPIFIQLVPGILQMYYEQGLEKPKF
 EIQLDPYCRLESPKVENFSVACKIHTVKIEHVSYTEKRYHSKTEVHEPDIEQMLKLGSNTSYHDFLDFLTVEELMKL
 PAVSKPKKNYEISLEIVDNFWGKVTEKGKFVESAVITQIYCLCFCVNGNLECFTLNDLLELPKRDESYEKDSEKKGI
 DILDYHFHKCVNQFEQESRIKVFPLDACRFEMLRFTLYNDNLPSLKSVVVVGAYVELQAFVNMASLAQRSSYAG
 SLRSCDNIRIHFVPSQWIKALWTMNLQRQKSLSAKMNRRACLGSLOQELESEPVQIQTGVSAYESAYQAVVWKIDRLPD
 KNSSLDPHCHLSYKLELGSDQEIPSDWYPFATVQFSVPDTCSARTEVRSLGVESDVQPQKHVQQRACYNIQPKLYRSVIE
 DVIEGVRNLFAEEGIEEQVLKDLKQLWETKVLQLSKATEDFFRNSIQSPLFTLQLPHSLHQTLQSTSASLVIAPGRTPSF
 TTAEGLTSNNSANFTFPGYPIHVPAGVTQTVSGHLYKVNVPIMVTETSGRAGILQHPIQQVFQQLGQPSVIQTSVPQLN
 PWSLQATTEKSQRIETVLLQQPAILPSGPVDRKHLENATSDILVSPGNEHKIVPEALLCHQESSHYISLPGVVFSPQVSQT
 NSDVEVLSGSASMAQNLHDESLSTSPHGALHQHVTDIQLHILKNRMYGCDSVKQPRNIEEPSNIPESEKDSNSQVDLSI
 RVTDDDIGEIIVQDGSGDTSSNEEIGSTRADADADENEFLGNIDGGDLKVPEEEADSISNEDSATNSSDNEDPQVNIVEEDPL
 NSGDDVSEQDVPDFDTDNIVCQYDKIHRSKNKWKFYLDGVCMFGGRDYVFAKAIGDAEW

Figure 4.

TRANSCRIPTION FACTORS RELATED TO TFIIA

TECHNICAL FIELD OF THE INVENTION

The present invention relates in general to the field of recombinant nucleic acids, polypeptides and other derived materials and, more particularly, to the identification, isolation and characterization of human transcription factors that are involved in the expression of human genes.

BACKGROUND OF THE INVENTION

Without limiting the scope of the invention, its background is described in connection with the isolation, characterization and use of human transcription factors that are expressed throughout the organism, as an example.

5 Unlike the nucleic acid polymerases of prokaryotes, purified RNA polymerase II from eukaryotes initiates transcription very poorly and essentially at random. One key difference between prokaryotic and eukaryotic polymerases is the need for accessory factors that provide for the accurate initiation of transcription. These factors are referred to as the "general" or "basal" transcription factors, in that they are required, in addition to RNA
10 polymerase II, for the transcription of all eukaryotic protein coding genes. As such, the general transcription factors are expected to be active, or at least present, in all or most tissues. One such general factor is called transcription factor IID (TFIID) and is responsible in large part for promoter recognition. Other general transcription factors include TFIIA, TFIIB, TFIIE, TFIIF and TFIIH.

15 Appropriate levels of gene- and tissue-specific transcription is achieved by another set of factors called activator proteins. These factors are often composed of two domains, a sequence-specific DNA recognition domain and an activation domain. When bound to DNA, the activation domain facilitates the formation and function of a preinitiation complex that consists of the general transcription factors and RNA polymerase II. In this way it is possible to direct the selective transcription of genes in an appropriately regulated fashion.
20

25 The structure of a typical promoter for a eukaryotic gene consists of two general regions. The core promoter is located at or near the actual site of transcription initiation and often includes a TATA sequence element located at about 30 base pairs upstream of the initiation site. The other regions are defined as sequence elements which are recognized by activator proteins. These are often located at various distances further upstream, but may be also be located downstream relative to the core promoter of the gene being regulated. Interactions between bound regulatory factors and the preinitiation complex are responsible for the precisely regulated transcription of each individual gene.

TFIIB is an essential general transcription factor and the purified factor from higher eukaryotes consists of three subunits, designated alpha (35 kD), beta (19 kD) and gamma (12 kD). In humans, the alpha and beta subunits are encoded by DNA sequences present in the TFIIB α/β cDNA, sometimes referred to as the 'large' subunit cDNA. These two subunits are post-translationally processed from a large 55 kD product of TFIIB α/β . The gamma subunit is encoded by DNA sequences present in the TFIIB γ cDNA, sometimes referred to as the 'small' subunit cDNA. This sequence is the subject of United States Letters Patent No. 5,562,117 issued to Moore and Rosen. TFIIB has multiple roles in transcription initiation by RNA polymerase II, including an ability to stabilize TBP-TATA element interactions, displace TBP-associated repressors and serve as a cofactor during the processes of transcription activation.

Most of the known human general transcription factors appear to be generally required in all tissues for gene expression by RNA polymerase II. Thus, these factors will be important as markers to evaluate disease states which may arise from inappropriately regulated gene expression and as pharmacological reagents and/or targets with which to modulate patterns of gene expression. Similarly, overexpression via gene therapy or other means should have broad effects on the expression of many or all cellular genes. In contrast, mutations in the genes for activator proteins, which are normally observed to control expression of a select set of genes, often in a tissue or developmentally restricted pattern, typically result in specific defects. Likewise, overexpression of activator proteins only affects expression of cellular genes which contain cognate recognition sequences.

Testis has important endocrine (hormonal) functions and is the site for the production of haploid spermatozoa from undifferentiated stem cells, a process called spermatogenesis. Mutations in some specialized transcriptional activator proteins, such as A-myb and CREM, cause male infertility and show defects in spermatogenesis. The identification of tissue-specific human general transcription factor would bridge an important gap between the generality for general transcription factor function and the specificity of gene-specific transcriptional activator protein function. If such factors were testis-specific, they would be expected to regulate patterns of gene expression that are important in the endocrine,

}

spermatogenic and other functions of this organ. The present invention satisfies a need in the art for new compositions for polynucleotide sequences and encoded polypeptide products, immunological reagents and other derived materials in terms of providing unique reagents for the detection of defects in testis function such as idiopathic male infertility or other syndromes, for detection of dysfunctional patterns of gene expression and as reagents that can modulate gene expression.

5

SUMMARY OF THE INVENTION

The present invention includes DNA sequences that encode two structurally distinct isoforms of the human general transcription factor TFIIA α/β . One of these sequences is denoted as ALF, for TFIIA α/β -like factor, which is expressed predominantly in human testis. The second sequence contains ALF connected to a unique upstream sequence and is denoted as SALF, for Stoned B/TFIIA α/β -like factor. The present invention is also direct to recombinant polypeptide products and other derived materials. The uses of the invention include, but are not necessarily limited to, the propagation and preparation of the ALF and SALF DNA, RNA and recombinant proteins, and use of these materials as reagents and markers to detect and/or modify the function of eukaryotic cells in normal and disease states.

The present invention may be used in the detection of the endogenous ALF and SALF RNAs in eukaryotic cells using hybridization, polymerase chain reactions, immunological analysis and other methods. The invention may also be used along with the endogenous ALF and SALF DNAs, RNAs and proteins as specific *in vivo* pharmacological targets to artificially modulate the expression of eukaryotic genes. Furthermore, the ALF, SALF and the variable carboxyl terminal end may be introduced in a normal or modified versions of the ALF and SALF genes for expression in eukaryotic cells in order to replace or augment endogenous transcription factor activities (gene therapy). The present invention may also be used as testis-specific antigens for contraceptive vaccine development.

The present invention, in a general and overall sense, concerns the isolation and characterization of a novel transcriptional factor gene, ALF and carboxy terminal variable region. One embodiment of the present invention is a purified nucleic acid segment that encodes a protein having an amino acid sequence as shown in Figure 2, in accordance with SEQ ID NO.:2. Another embodiment of the present invention is a purified nucleic acid segment, further defined as including a nucleotide sequence in accordance with SEQ ID NO.:1.

The present invention also concerns the isolation and characterization of a novel transcriptional factor gene, SALF and a carboxy terminal variable region. One embodiment of the present invention is a purified nucleic acid segment that encodes a protein having an

amino acid sequence as shown in Figure 3, in accordance with SEQ ID NO.:4. Another embodiment of the present invention is a purified nucleic acid segment, further defined as including a nucleotide sequence in accordance with SEQ ID NO.:3. The 3' variable region that ALF and SALF have in common is encoded by the nucleic acid segment in accordance with SEQ ID NO.:5 and expressed as an amino acid sequence as shown in SEQ ID NO.:6.

In one embodiment the purified nucleic acid segment includes the nucleotide sequence of SEQ ID NOS.:1, 3 and 5. As used herein, the term "nucleic acid segment" and "DNA segment" are used interchangeably and refer to a DNA molecule that has been isolated free of total genomic DNA of a particular species. Therefore, a "purified" DNA or nucleic acid segment as used herein, refers to a DNA segment that includes novel transcriptional factor genes, ALF, SALF and a carboxy terminal variable coding sequence, yet is isolated away from, or purified free from, total genomic DNA, for example, total cDNA or human genomic DNA. Included within the term "DNA segment", are DNA segments and smaller fragments of such segments and recombinant vectors, including, for example, plasmids, 10 cosmids, phage, viruses and the like.

Similarly, a DNA segment encoding an isolated or purified novel transcriptional factor genes, ALF, SALF and a carboxy terminal variable coding sequence, gene refers to a DNA segment including ALF, SALF and a carboxy terminal variable coding sequence isolated substantially away from other naturally occurring genes or protein encoding sequences. In this respect, the term "gene" is used for simplicity to refer to a functional protein, polypeptide or peptide encoding unit. As will be understood by those in the art, this functional term includes both genomic sequences, cDNA sequences or combinations thereof. "Isolated substantially away from other coding sequences" means that the gene of interest, in this case ALF, SALF and a carboxy terminal variable coding sequence, forms the significant part of the coding region of the DNA segment. Of course, this refers to the DNA segment as originally isolated and does not exclude genes or coding regions later added by the hand of man to the segment.

In particular embodiments, the invention concerns isolated DNA segments and recombinant vectors incorporating DNA sequences that encode novel transcriptional factor

genes, ALF, SALF and a carboxy terminal variable coding sequence genes, and that include within the amino acid sequence an amino acid sequence in accordance with SEQ ID NO.:2. Moreover, in other particular embodiments, the invention concerns isolated DNA segments and recombinant vectors incorporating DNA sequences that encode a gene which includes within its amino acid sequence the amino acid sequence of a ALF, SALF and a carboxy terminal variable coding sequence

Another embodiment of the present invention is a purified nucleic acid segment that encodes proteins in accordance with SEQ ID NOS.:2, 4 and 6, further defined as a recombinant vectors. As used herein the term, "recombinant vector", refers to a vector that has been modified to contain a nucleic acid segment that encodes ALF, SALF, or the carboxy terminal variable coding sequence protein, or a fragment thereof. The recombinant vector may be further defined as an expression vector that includes a promoter operatively linked to the ALF, SALF, or the ALF/SALF variants having the carboxy terminal variable coding sequence encoding a nucleic acid segment.

A further embodiment of the present invention is a host cell, made recombinant with a recombinant vector including ALF, or SALF, and if present, a carboxy terminal variable coding sequence. The recombinant host cell may be a prokaryotic cell. In a one embodiment, the recombinant host cell is a eukaryotic cell. As used herein, the term "engineered" or "recombinant" cell is intended to refer to a cell into which a recombinant gene, such as a gene encoding ALF, SALF, or the carboxy terminal variable coding sequence, has been introduced. Therefore, engineered cells are distinguishable from naturally occurring cells which do not contain a recombinantly introduced gene. Engineered cells are thus cells having a gene or genes introduced through the hand of man. Recombinantly introduced genes will either be in the form of a cDNA, a copy of a genomic gene, or will include genes positioned adjacent to a promoter not naturally associated with the particular introduced gene.

It may be more convenient, however, to employ as the recombinant gene a cDNA version of the gene. One advantage of working with cDNAs is that the size of the gene is generally smaller and more readily employed to introduce into or "transfect" the targeted cell

than will a genomic gene; typically an order of magnitude larger than cDNA gene. Alternatively, a genomic version of a particular gene may be used where desired.

In certain embodiments, the invention concerns isolated DNA segments and recombinant vectors that encode a protein or peptide which includes within its amino acid sequence an amino acid sequence essentially as set forth in SEQ ID NOS.:2, 4 or 6. Naturally, where the DNA segment or vector encodes a full length ALF or Salf protein, or is intended for use in expressing the sequences will be as essentially as set forth in SEQ ID NOS.:2, 4 and 6.

The term "a sequence essentially as set forth in SEQ ID NO.:2" means that the sequence substantially corresponds to a portion of SEQ ID NO.:2 and has relatively few amino acids which are not identical to, or a biologically functional equivalent of, the amino acids of SEQ ID NO.:2. Likewise the phrase is equally applied to SEQ ID NOS.: 4 and 6. The term "biologically functional equivalent" is well understood in the art and is further defined in detail herein as a gene having a sequence essentially as set forth in SEQ ID NOS.:2, 4 or 6, and that is associated with RNA transcription. Accordingly, sequences that have between about 70% and about 80%; or between about 81% and about 90%; or even between about 91% and about 99%; of amino acids that are identical or functionally equivalent to the amino acids of SEQ ID NOS.:2, 4 or 6.

In certain other embodiments, the invention concerns isolated DNA segments and recombinant vectors that include within their sequence a nucleic acid sequence essentially as set forth in SEQ ID NOS.:1, 3 or 5. The term "essentially as set forth in SEQ ID NO.: 1," is used in the same sense as described above and means that the nucleic acid sequence substantially corresponds to a portion of SEQ ID NO.:1, and has relatively few codons that are not identical, or functionally equivalent, to the codons of SEQ ID NO.:1. Likewise the phrase is equally applied to SEQ ID NOS.: 3 and 5. The functionally equivalent codons are known in the art.

It will also be understood that amino acid and nucleic acid sequences may include additional residues, such as additional N- or C-terminal amino acids or 5' or 3' sequences, and yet still be essentially as set forth in one of the sequences disclosed herein, so long as the

sequence meets the criteria set forth above, including the maintenance of biological protein activity where protein expression is concerned. The addition of terminal sequences particularly applies to nucleic acid sequences that may, for example, include various non-coding sequences flanking either of the 5' or 3' portions of the coding region or may include various internal sequences, i.e., introns, which are known to occur within genes.

Excepting intronic or flanking regions, and allowing for the degeneracy of the genetic code, sequences that have between about 70% and about 80%; or between about 80% and about 90%; or between about 90% and about 99%; of nucleotides that are identical to the nucleotides of SEQ ID NOS.:1, 3 or 5 will be sequences that are "essentially as" the respective SEQ ID NOS. Sequences that are essentially the same as those set forth in SEQ ID NOS.:1, 3 or 5 may also be functionally defined as sequences that are capable of hybridizing to a nucleic acid segment containing the complement of SEQ ID NO.:1 under relatively stringent conditions. Suitable relatively stringent hybridization conditions will be well known to those of skill in the art and are clearly set forth herein, for example conditions for use with southern and northern blot analysis as described herein.

Naturally, the present invention also encompasses DNA segments that are complementary, or essentially complementary, to the sequence set forth in SEQ ID NOS.:1, 3 or 5. The nucleic acid segments of the present invention, regardless of the length of the coding sequence itself, may be combined with other DNA sequences, such as promoters, polyadenylation signals, additional restriction enzyme sites, multiple cloning sites, other coding segments, and the like, such that their overall length may vary considerably. A nucleic acid fragment of almost any length may be employed, with the total length being limited by the ease of preparation and use in the intended recombinant DNA protocol. For example, nucleic acid fragments may be prepared that include a short stretch complementary to SEQ ID NOS.:1, 3 or 5, such as about 10 to 15 or 20, 30, or 40 or so nucleotides, and which are up to 10,000 or 5,000 base pairs in length, with segments of 3,000 being used in certain cases. DNA segments with total lengths of about 1,000, 500, 200, 100 and about 50 base pairs in length are also useful.

Another embodiment of the present invention is a nucleic acid segment that includes at least a 14-nucleotide long stretch that corresponds to, or is complementary to, the nucleic acid sequence of SEQ ID NOS.:1, 3 or 5. In one embodiment the nucleic acid is further defined as including at least a 20, 30, 50, 100, 200, 500, 1000, or at least a 3824 nucleotide long stretch that corresponds to, or is complementary with, the nucleic acid sequence of SEQ ID NOS.:1, 3 or 5. The nucleic acid segment may be further defined as having the nucleic acid sequence of SEQ ID NOS.:1, 3 or 5.

A related embodiment of the present invention is a nucleic acid segment that includes at least a 14-nucleotide long stretch that corresponds to, or is complementary with, the nucleic acid sequence of SEQ ID NO.:1 or 3, further defined as including a nucleic acid fragment of up to 10,000 base pairs in length. Another embodiment is a nucleic acid fragment including from 14 nucleotides of SEQ ID NO.:1 or 3 up to 5,000, 3,000, 1,000, 500 or 100 base pairs in length.

Naturally, it will also be understood that this invention is not limited to the particular nucleic acid and amino acid sequences of SEQ ID NOS.: 2, 4 and 6. Recombinant vectors and isolated DNA segments may therefore variously include the ALF, SALF and variable region coding regions themselves, coding regions bearing selected alterations or modifications in the basic coding region, or they may encode larger polypeptides that nevertheless include ALF, SALF or variable region-coding segments or may encode biologically functional equivalent proteins or peptides that have variant amino acids sequences.

The DNA segments of the present invention encompass biologically functional equivalent ALF, SALF and variable region peptides. Such sequences may arise as a consequence of codon redundancy and functional equivalency that are known to occur naturally. Alternatively, functionally equivalent proteins or peptides may be created via the application of recombinant DNA technology, where changes in the protein structure may be engineered, based on considerations of the properties of the amino acids being exchanged. Changes designed by man may be introduced through the application of site-directed mutagenesis techniques, e.g., to introduce improvements to the antigenicity of the ALF,

SALF or variable region mutants in order to examine transcriptional activity or determine the presence of ALF, SALF or variable region protein in various cells and tissues at the molecular level.

Another embodiment of the present invention is a purified composition comprising
5 a polypeptide having an amino acid sequence in accordance with SEQ ID NOS.:2, 4 or 2 or 4 with 6. The term "purified" as used herein, refers to a transcriptional factor protein composition, wherein the ALF, SALF or ALF and SALF having the variable region proteins are purified to any degree relative to its naturally-obtainable state, i.e., in this case, relative to its purity within a eukaryotic cell extract, or a testis sample. A cell for the isolation of
10 ALF, SALF or variants thereof is a cell of testicular origin, however, these proteins may also be isolated from patient specimens, recombinant cells, tissues, isolated subpopulations of tissues, and the like, as will be known to those of skill in the art, in light of the present disclosure. Purified ALF, SALF or variants thereof also refer to polypeptides having the amino acid sequence of SEQ ID NOS.:2, 4, 2 and 6 or 4 and 6, free from the environment
15 in which it may naturally occur. One may also prepare fusion proteins and peptides, e.g., where the ALF, SALF or variable portion coding regions are aligned within the same expression unit with other proteins or peptides having desired functions, such as for purification or immunodetection purposes (e.g., proteins that may be purified by affinity chromatography and enzyme label coding regions, respectively).

20 Turning to the expression of ALF, SALF and variable genes whether from cDNA or genomic DNA, protein may be prepared using an expression system to make recombinant preparations of ALF, SALF and variable genes proteins. The engineering of DNA segment(s) for expression in a prokaryotic or eukaryotic system may be performed by techniques generally known to those of skill in recombinant expression. For example, ALF,
25 SALF and variable genes-GST (glutathione-S-transferase) fusion proteins are a convenient means of producing protein in a bacterial expression. Virtually any expression system may be employed in the expression of ALF, SALF and variable gene products. Eukaryotic expression systems, however, may also be used.

Transformation of host cells with DNA segments encoding ALF, SALF and variable genes also provides a convenient means for obtaining a protein for ALF, SALF and ALF or SALF including the variable portions. Complementary DNA (cDNA), genomic sequences and combinations thereof, are suitable for eukaryotic expression, as the host cell will, of course, process the genomic transcripts to yield functional mRNA for translation into protein.

Another embodiment is a method of preparing a protein composition comprising growing recombinant host cell comprising a vector that encodes a protein that includes an amino acid sequence in accordance with SEQ ID NOS.:2, 4 or 6, under conditions permitting nucleic acid expression and protein production followed by recovering the protein so produced. The host cell, conditions permitting nucleic acid expression, protein production and recovery, will be known to those of skill in the art, in light of the present disclosure of the ALF, SALF and variable region genes.

BRIEF DESCRIPTION OF THE DRAWINGS

For a more complete understanding of the features and advantages of the present invention, reference is now made to the detailed description of the invention along with the accompanying figures which corresponding numerals in the different figures refer to the corresponding parts and in which:

5 FIG. 1 depicts the cDNA sequence of ALF (SEQ ID NO. 1);

FIG. 2 depicts the corresponding deduced amino acid sequence of ALF (SEQ ID NO. 2), standard one-letter abbreviations for amino acids is used;

10 FIG 3 depicts the cDNA sequence of SALF (SEQ ID NO. 3);

FIG 4 depicts the corresponding deduced amino acid sequence of ALF (SEQ ID NO. 4), standard one-letter abbreviations for amino acids is used;

15 FIG 5 depicts the cDNA sequence of an alternative 3'-coding and untranslated region for both ALF and SALF (SEQ ID NO 5);

FIG 6 depicts the corresponding deduced amino acid sequence of ALF (SEQ ID NO. 6), standard one-letter abbreviations for amino acids is used;

20 FIG 7A and 7B depicts the schematic structures of the ALF and SALF cDNA sequences. A, The SALF cDNA sequence includes TFIIA α/β -like sequences and an upstream Stoned β -like region and is shown with selected restriction enzyme sites. B, The ALF cDNA sequence consists of TFIIA α/β -like sequences. The 5'-end of ALF was identified using gene-specific primers 2a2-20 and 2a2-22 and library-specific primers AP1 and AP2. The resulting clone, pRACE22, is shown as a single line. A PCR product that spans the entire ALF sequence (pRACE17) was obtained using gene-specific primer 2a2- 17 and library-specific primer AP1. C, PCR products from SALF are amplified and visualized from human placenta and liver cDNA libraries. The primers used are indicated above each lane (2a2-1, 2a2-6 and 2a2-8). Lanes 5 and 6 are control reactions to which no cDNA template was added;

25 FIG 8A and 8B are schematic diagrams showing alignments of ALF and SALF sequences with related genes. A, ALF contains conserved regions I, III and IV and an internal nonconserved region II. Beneath ALF are diagrams of TFIIA large subunits from

human (hTFIIA α/β), Arabidopsis (aTFIIA-L), Drosophila (dTFIIA-L) and yeast (yTOA1). B, A diagram of the N-terminus of SALF is shown, indicating an upstream serine, threonine, a proline-rich domain and a downstream domain that is homologous to Drosophila Stoned β and the clathrin APs $\mu 1$ (AP47) and $\mu 2$ (AP50) proteins.

5 FIG. 9 shows human genomic DNA digested with either BglII or EcoRI and hybridized with an ALF probe. The enzymes are indicated above each lane (lanes 1 BglII; lanes 2, EcoRI). The positions of the molecular weight size markers are indicated to the left of each panel.

10 FIG 10A through 10E are Northern blot analysis autoradiographs of ALF, TFIIA α/β and TFIIA γ transcripts. Poly(A) mRNA from various human tissues were probed with various gene-specific probes. A, ALF; B, 5'-SALF; C, TFIIA α/β ; D, TFIIA γ ; and E, actin.

15 FIG 11A through 11F are RNA dot blot analyses autoradiographs of ALF, TFIIA α/β and TFIIA γ transcripts; A single dot blot containing poly(A) mRNA from multiple human tissues is probed with A, ALF, B, 5'-SALF, C, TFIIA α/β , D, TFIIA γ ; and E, a ubiquitin control. The source of the mRNA for each spot is listed in F, dashes indicate positions that do not contain mRNA.

20 FIG 12A through 12D show expression and functional analysis of ALF and SALF polypeptides. A, Coomassie-stained SDS-PAGE gel shows that the recombinant histidine-tagged ALF protein migrates at 69 kD (lane 2) and that the recombinant rat TFIIA α/β and TFIIA γ proteins used in these studies migrate at 55 kD and 12 kD, respectively (lanes 3 and 4). B, p69 (ALF) can substitute for (TFIIA α/β) p55 in stabilizing the interaction between TBP and the Adenovirus Major Late promoter TATA element (-40 to -16). Additions to each reaction are listed above each lane. Polyclonal antiserum against human p55 is added to reactions in lanes 8 (2 μ l), 9 (4 μ l) and 10 (4 μ l). C, Addition of p69 (ALF) and p12 (TFIIA γ) restore activity to transcriptionally inactive TFIIA-depleted HeLa nuclear extracts. Control (undepleted) and TFIIA-depleted extracts are indicated by a "C" and "D", respectively. D, A T7-promoter driven SALF construct produces an [35S]-labeled protein of approximately 170 kD in in vitro transcription- translation reactions.

DETAILED DESCRIPTION OF THE INVENTION

While the making and using of various embodiments of the present invention are discussed in detail below, it should be appreciated that the present invention provides many applicable inventive concepts which can be embodied in a wide variety of specific contexts. The specific embodiments discussed herein are merely illustrative of specific ways to make and use the invention and do not delimit the scope of the invention.

Human transcription factor IIA (TFIIA) is a cellular factor that, together with additional protein components, regulates the expression of human genes. TFIIA is composed of proteins produced from two nucleic acid sequences (genes), one called hTFIIA α/β and the other hTFIIA γ (Patent No. 5,652,117). These factors are expressed in human tissues and are thought to function primarily through interactions with the TATA-binding protein (TBP), a universally-required eukaryotic protein that functions at promoter DNA sequences to regulate gene expression.

In addition to the DNA sequences themselves, the functionality of the recombinant polypeptides produced from the ALF DNA sequences is shown using several biochemical assays. First, in conjunction with a recombinant TFIIA γ polypeptide, the recombinant ALF protein overproduced and purified from *E. coli*, can interact with recombinant human TATA binding protein to stabilize interactions on promoter DNA. Second, in conjunction with a recombinant TFIIA γ polypeptide, the recombinant ALF polypeptide can restore RNA polymerase II transcription activity to nuclear extracts from human cells that have been depleted of TFIIA. Related, antibody reagents raised against the recombinant ALF polypeptides react with the corresponding overproduced polypeptides suggesting that immunological detection of the endogenous protein(s) will be feasible. These studies substantiate the prediction that the ALF protein has a role in the regulation of human gene expression.

DEFINITIONS

As used throughout the present specification the following abbreviations are used: TF, transcription factor; TBP, TATA binding protein; ORF, open reading frame, EST,

expressed sequence tag; kb, kilobase (pairs); UTR, untranslated region; kD, kilodalton; nt, nucleotide; aa, amino acids; bp, base pairs; PCR, polymerase chain reaction; AP, adaptor protein; DTT, dithiothreitol; PMSF, phenylmethylsulfonyl flouride; EDTA, ethylenediaminetetraacetic acid; IPTG, isopropyl β -D-thiogalactoside; AdML, Adenovirus Major Late; ALF, TFIIA α/β -like factor; SALF, Stoned B/ TFIIA α/β -like factor.

5 Terms defined herein have meanings as commonly understood by a person of ordinary skill in the areas relevant to the present invention. Terms such as "a", "an" and "the" are not intended to refer to only a singular entity, but include the general class of which a specific example may be used for illustration. The terminology herein is used to describe 10 specific embodiments of the invention, but their usage does not limit the invention, except as outlined in the claims.

The term "ALF" (TFIIA α/β -like factor) refers to the nucleotides essentially as set forth (SEQ ID NO. 1) or amino acid sequences essentially as set forth (SEQ ID NO 2). The term "SALF" (Stoned B/TFIIA α/β -like factor) refers to the nucleotides essentially as set 15 forth (SEQ ID NO.3) or amino acid sequence essentially as set forth (SEQ ID NO. 4). The term "alternative carboxy terminal domain" refers to nucleotide essentially as set forth (SEQ ID NO. 5) and amino acid sequences essentially as set forth (SEQ ID NO. 6) It is to be understood that alternative carboxy terminal sequence is present as an alternative 3'-coding and untranslated region that can be found on some ALF or SALF transcripts or cDNAs and 20 is meant to be included or implied in all references to the term "ALF and SALF", without referring to this alternative sequence explicitly each time.

The terms "a sequence essentially as set forth in SEQ ID NO. (#)", "a sequence similar to", "nucleotide sequence" and similar terms, with respect to nucleotides, refers to 25 sequences that substantially correspond to any portion of the sequences in SEQ ID NOS 1, 3 and 5. These terms refer to synthetic as well as naturally-derived molecules and includes sequences that possess biologically, immunologically, experimentally, or otherwise functionally equivalent activity, for instance with respect to hybridization by nucleic acid segments, or the ability to encode all or portions of ALF or SALF activities. Naturally, these terms are meant to include information in such a sequence as specified by its linear order.

The terms "a sequence essentially as set forth in SEQ ID NO. (#)", "a sequence similar to", "amino acid sequence" and similar terms, with respect to amino acids, refers to peptides, polypeptides, proteins, fragments, fusions, derivatives and alterations thereof that substantially correspond to any portion of the sequences in SEQ ID NOS. 2, 4 and 6. These terms refer to synthetic as well as naturally-derived molecules and includes sequences that possess biologically, immunologically, experimentally, or otherwise functionally equivalent activities, for instance, segments of amino acids which possess immunological activity as an antigenic determinant. Naturally, these terms are meant to include information in such a sequence as specified by its linear order.

The term "homology" and "similarity" refers to the extent to which two nucleic acids are complementary. The term "gene" is used to refer to a functional protein, polypeptide, or peptide encoding unit. As will be understood by those in the art, this functional term includes both genomic sequences, cDNA sequences, or fragments or combinations thereof, as well as gene products, including those that may have been altered by the hand of man.

The term "biologically equivalent" or "functionally equivalent" are understood in the art and is further defined herein as sequences that are interchangeable or similarly useful with reference to a given property, for instance selectivity of hybridization, or which encode amino acid segments that have similar properties.

The term "vector" refers to DNA or RNA sequences that have been modified to contain a nucleic acid segment that encodes ALF or SALF, or a fragment thereof. The vector may be further defined as one designed to propagate ALF and SALF sequences, or as an expression vector that includes a promoter operatively linked to the ALF or SALF sequences, or one designed to cause such a promoter to be introduced. The vector may exist in a state independent of the host cell chromosome, or may be integrated into the host cell chromosome

The term "host cell" refers to cells that have been engineered to contain nucleic acid segments from ALF or SALF, or altered segments, whether archeal, prokaryotic, or eukaryotic. Thus, engineered, or recombinant cells, are distinguishable from naturally occurring cells that do not contain recombinantly introduced genes through the hand of man.

5 The term "agonist" refers to a molecule that enhances either the strength or the time of an effect of ALF or SALF and encompasses small molecules, proteins, nucleic acids, carbohydrates, lipids, or other compounds. The term "antagonist" refers to a molecule that decreases either the strength or the time of an effect of ALF or SALF and encompasses small molecules, proteins, nucleic acids, carbohydrates, lipids, or other compounds.

10 The term "altered" or "alterations", or "modified" with reference to nucleic acid or polypeptide sequences is meant to include changes such as insertions, deletions, substitutions, fusions with related or unrelated sequences, such as might occur by the hand of man, or those that may occur naturally such as polymorphisms, alleles and other structural types. Alterations encompass genomic DNA and RNA sequences that may differ with respect to their hybridization properties using a given hybridization probe. Alterations of polynucleotide sequences that encode ALF or SALF, or fragments thereof, include those that increase, decrease, or have no effect on functionality. Alterations of polypeptides refer to those that have been changed by recombinant DNA engineering, chemical, or biochemical modifications, such as amino acid derivatives or conjugates, or post-translational modifications.

15

The term "antibody" refers to any of a class of immunological molecules with the capacity to interact specifically with one or more epitopes of ALF or SALF and includes those that have been altered or modified, for example, 'humanized' antibodies.

20 The term "complementary" refers to polynucleotide sequence that may form stable base pairs with another sequence under a given set of conditions. For instance a complementary strand refers to a sequence that is a sequence of nucleotides whose composition is dictated by the Watson-Crick base pairs (A-T, G-C). This term also refers to any polynucleotide sequence that can selectively interact with another under either permissive or stringent hybridization conditions, as known to those skilled in the art and, in this respect, includes sequences of DNA or oligonucleotides, RNA, protein nucleic acid, other nucleic acid derivatives and fragments thereof, which can reliably detect a particular sequence with a specificity that is useful for genetic or diagnostic studies.

25

The term "modulate" refers to the ability to effect a change in the structure, function, or regulation of ALF or SALF genes or gene products. These include methods for altering ALF or SALF gene activity and protein function.

5 The terms "segment", "fragment", "portion", "part", "region", or "domain", refers to any subsections, regardless of length, of nucleotide or amino acid sequences set forth in this invention that are either whole or which have been divided either naturally or by the hand of man.

10 The term "oligonucleotide probe" or "oligonucleotide primer" refers to a polynucleotide sequence between approximately 6 nucleotides to 70 to 80 nucleotides, but typically between 15-30 nucleotides, that can be used in direct hybridization, including microarray techniques, or in amplification assays to achieve a substantially selective detection of a complementary sequence. Such sequences are used for a wide variety of additional purposes, the basis of which is the relatively selective annealing to a particular target complementary nucleic acid sequence.

15 The term "sample" refers to any biochemical or biological specimen that is typically being analyzed for some property, for instance biological or biochemical activity of ALF or SALF, presence or absence of ALF or SALF protein, nucleic acid, including any alteration in the normal distribution or structure of these genes or encoded products. Samples may include, but are not limited to, cells and cell extracts or extracts thereof, including protein and membrane fractions, chromosomes, genomic DNA, RNA, cDNA and so forth, regardless 20 of the particular state of isolation.

25 The term "stringent hybridization conditions" refers to an setting in which two polynucleotide sequences are hybridized under conditions that favor specific over nonspecific interactions. For instance, stringent hybridization conditions might include combinations of salt, organic reagents, blocking agents, detergents, temperature and so forth that allow for hybridization between highly similar sequences, such as those related by 95% or greater identity over a length of sequence sufficient for stable hybridization. The term "hybridization" also refers to complementary interactions between a polynucleotide sequence and an oligonucleotide, and may be performed under conditions of varying stringency that

would be dictated by length and homology of the oligonucleotide(s) used and would be determined by one skilled in the art without undue experimentation.

The term "permissive hybridization conditions" refers to an setting in which two polynucleotide sequences are hybridized under conditions in that polynucleotide sequences with less similarity, for instance as low as 50-60%, are caused to interact. For instance, permissive hybridization conditions might include combinations of salt, organic reagents, blocking agents, detergents, temperature, and so forth that allow for stable hybridization, but may allow a greater degree of nonspecific, or background, hybridization than would be observed under stringent conditions. Hybridization between less related sequences is also facilitated by the use of nucleotides such as inosine within hybridizing nucleic acid segments.

The term "transformation" refers to any means by which DNA or RNA is caused to enter a recipient, or host, chromosome, cell, or organism.

The term "detection" refers to the ability to selectively detect a particular biological or biochemical compound. Detection of polynucleotide sequences in a sample, or the levels of such sequences in a sample, is often achieved by hybridization with a complementary polynucleotide or oligonucleotide sequence, or by amplification. Detection of polypeptides is often achieved on the basis of immunological recognition with antigen specific antibodies. Detection of biological or biochemical activity is often achieved by assaying a sample for an activity that is possessed by the compound being assayed.

The term "amplification" refers to the production of multiple copies of a given polynucleotide sequence. Amplification can be achieved as the growth of a vector contained within a host cell. Alternatively, the amplification of specific DNA, or reverse transcribed RNA, sequences that lie between two oligonucleotide primers can be achieved through the polymerase chain reaction, as known in the art.

The term "purified" or "isolated" with reference to DNA or other nucleic acid segment, or amino acid segment, refers to a sequence that includes novel transcription factor genes ALF and SALF, yet is isolated substantially away from, or purified substantially away from total genomic DNA, total cDNA, total or poly(A) RNA, total cellular, subcellular, or tissue extract, or other populations of molecules.

The term "ligand" refers to any molecule, whether nucleic acid, amino acid, or other chemical compositions that interacts with ALF or SALF.

INTRODUCTION

5 The synthesis of accurately-initiated messenger RNA in eukaryotic organisms requires the assembly of RNA polymerase II and the general transcription factors (TFIIA, B, D, E, F and H) at core promoters (1, 2). Human TFIIA is composed of 35 (a), 19 (b) and 12 (g) kD subunits encoded by the hTFIIA α/β (3, 4) and hTFIIA γ (5-7) (Patent No. 5,652,117) cDNAs and evolutionarily conserved cDNAs have been characterized in yeast (yTOA1 and yTOA2) (8) and Drosophila (dTFIIA-L and dTFIIA-S) (9-11). The human TFIIA subunits are expressed in all or most human tissues and are thought to function primarily through interactions with the TATA-binding protein (TBP), a universally required eukaryotic protein that functions a promoter sequences to facilitate and regulate gene expression.

15 TFIIA has multiple roles in transcription initiation by RNA polymerase II. First, TFIIA stabilizes the TBP-TATA element interaction (14-17). TFIIA also stimulates transcription by displacing TBP-associated repressors such as Dr1/NC2, Dr2/Topo1, HMG1 and DSP1 (18-22) and counteracts the ability of ADI/MOT1, hTAFII172, yTAFII145 and hTAFII250 to inhibit TBP binding to DNA (23-27). Second, TFIIA serves as a cofactor for the AP-1, Gal4-AH, Zta, VP16, CTF, NTF and Sp1 activators (4-7, 10, 28-31) and for the PC4 and HMG-2 coactivators (32, 33). Third, TFIIA is required for the isomerization and extension of TFIID-promoter contacts (34, 35) and for stabilizing interactions between TFIID and initiator sequences (36).

20 One of the nucleic acid sequences disclosed herein is called SALF (Stoned B/TFIIA α/β -like factor). SALF is composed of both Stoned B/clathrin AP-like and TFIIA α/β -like sequences. An initial incomplete SALF sequence was recognized in NCBI database queries using TFIIA α/β sequence query by the inventor as an expressed sequence tag (EST) DNA sequence (ID 259637) described by the I.M.A.G.E. consortium (37). Characterization and isolation of additional sequences by the inventor has revealed a composite 3,853 bp cDNA sequence (FIG 3) that contains a 114 nucleotide 5'-UTR and a

161 nucleotide 3'-UTR with a poly(A) addition signal and a 29 nucleotide poly(A) tract. The deduced ORF commences with a putative start codon (AAGATGT) that is preceded by an in-frame stop codon 27 nucleotides upstream and predicts a 1,182-residue polypeptide (FIG 4) with a molecular weight of 132 kD and pI of 5.1.

5 Another new DNA sequence described herein is called ALF, for TFIIA α / β -like factor. ALF is isolated by PCR from a human testis cDNA library and is described as a 1,617 bp cDNA (FIG 1) that predicts a 478 amino acid polypeptide (FIG 2) with a molecular weight of 52 kD and pI of 4.4. ALF contains a 15 nt UTR, a putative initiation codon (GTCATGG) that conforms to the Kozak consensus (A/G NNATGG) (38) and 17 bp downstream of the ATG that predict six amino acids (ACLNPV) not present in SALF. ALF is expressed predominantly, if not exclusively, in testis (FIG 10A). Two additional new sequences that contain partial ALF-like sequences connected at nucleotide 1,344 to an alternative 261 bp 3'-end (FIG 5) are identified (I.M.A.G.E. Consortium CloneIDs 785133 and 1657721). These sequences predict a C-terminus in which the last 35 amino acids of ALF are replaced with the residues "AFPRRTSFNT" (FIG 6) followed by a stop codon and a 3'-UTR that contains a poly(A) addition signal and a poly(A) tail. PCR analysis has verified that both ALF and SALF cDNAs which contain this alternative 3'-end are present and can be PCR amplified, from human cDNA libraries. Importantly, none of the sequences disclosed herein have been previously reported, except as partial I.M.A.G.E. Consortium ESTs and as products of the inventor's work as currently disclosed and their intact sequences, structures, functions, uses and other characteristics.

10
15
20
25 A schematic comparison of ALF and other TFIIA large subunit sequences from human (3, 4), Drosophila (9), Arabidopsis (Genbank Accession number X98861) and yeast (8) is shown in FIG 8A. These sequences share a common organization consisting of conserved regions I and IV, acidic region III and an internal nonconserved region II. ALF is similar to its human TFIIA α / β counterpart in region I (aa 1-54; 67%) and region IV (aa 417-478; 73%) and in the negatively-charged region III (aa ~340-414; 42% D/E residues). In contrast, region II shares no homology with the corresponding region in hTFIIA α / β (or other TFIIA large subunits) and is approximately 100 residues longer. The unique

N-terminus of SALF is 711 amino acids in length (FIG 8B) and contains a region between amino acids 44 to 150 that is rich in proline (20%), serine (21%) and threonine (9%) residues. Residues between 275 and 692 display 47% similarity to the Drosophila Stoned B protein (39) and 46% similarity to an uncharacterized Stoned β -like ORF in C. elegans, C27H6.1 (53). The Drosophila stoned locus was first identified as a class of mutations that caused neurological defects such as temperature-sensitive paralysis (41) and it has been suggested that Stoned B functions in membrane trafficking in neurons (39). In addition, residues from 410 to 692 within the Stoned B-homology region are 33% and 37% similar to the mouse μ 1 (AP47) and rat μ 2(AP50) clathrin APs, respectively (FIG 7B) (42, 43). The μ 1 (AP47) and μ 2 (AP50) clathrin APs are subunits of the AP-1 and AP-2 complexes associated with the trans-Golgi and plasma membranes, respectively and function in the internalization, sorting and recycling of receptors and other membrane proteins (44, 45). Thus, the N-terminus of SALF is related to a family of proteins involved in membrane trafficking.

15

ALF AND SALF GENES

One aspect of the present invention is the polynucleotide sequences essentially as set forth as SEQ ID NOS. 1, 3 and 5, and in FIGS. 1 and 3, the complement of these sequences, the RNA versions of both DNA strands and the information otherwise contained within the linear sequence of these polynucleotide sequences and fragments thereof. In the case of nucleic acid segments, sequences for use with the present invention are those that have greater than about 50 to 60% homology with any portion of the polynucleotide sequences described herein, sequences that have between about 61% and about 70%; sequences that have between about 71 and about 80%; or between about 81% and about 90%; or between 20 91% and about 99%; or which contain nucleotides that are identical, functionally equivalent, or functionally irrelevant, with respect to the nucleotides present in SEQ ID NOS 1, 3 and 5 are considered to be essentially similar. Also encompassed within the present invention are nucleic acids that encode polypeptides that are at least 40% identical or similar to the amino acid sequences shown in SEQ ID NOS. 2, 4 and 6, and in FIGS. 2, 4 and 6.

The invention also encompasses other nucleic acids or nucleic acid like molecules that are sufficient in any regard to mimic, substitute for, or interfere with the ALF or SALF polynucleotide sequences or fragments thereof. It will also be understood that the nucleic acid and amino acid sequences may include additional residues, such as additional 5'- or 3'- sequences, and yet still be essentially as set forth in one of the sequences disclosed herein, so long as the sequence meets the criteria set forth, including the maintenance of functionality, or for the purpose of engineering altered functionality with respect to ALF and SALF.

Included within the invention are DNA or RNA segments including oligonucleotides, polynucleotides and fragments thereof, including DNA or RNA or nucleic acid-like sequences of genomic or synthetic origin, single or double stranded. The invention includes nucleic acid molecules, or nucleic acid-like molecules that are able to hybridize to the sequences in SEQ ID NOS. 1, 3 and 5, under stringent or under permissive hybridization conditions, or to the complement of said sequences.

The invention also includes oligonucleotide, or oligonucleotide-like sequences such as phosphothioates, or peptide nucleic acid sequences, that possess sufficient similarity with the sequences disclosed herein such that they are able to stably hybridize to the disclosed sequences, or their complements. Such sequences may be intended as antisense regulators of gene expression, or for the selective amplification or extension of adjoining sequences, for instance by PCR using a given annealing temperature, as would be determined by someone skilled in the art.

In addition to the sequences disclosed here, related sequences in other organisms, or homologs, will be readily identified by hybridization using the present sequences. This will facilitate the development of animal models for understanding disorders related to the overexpression, underexpression, or expression of forms with altered functionality, with respect to ALF, SALF, and similar sequences. Thus, related genes, and related mRNA transcripts, can be identified by one skilled in the art. The invention thus encompasses methods for the use of the disclosed sequences in various screening procedures aimed at isolating such species. For instance, colony or plaque hybridization techniques can be

performed using radiolabeled sequences as a probe to detect complementary sequences in genomic and cDNA libraries.

Hybridization conditions with respect to temperature, formamide and salt concentrations, in such studies are chosen by one skilled in the art and vary with respect to the organism from which sequences are being isolated, and the sequence similarity, or lack thereof, that is expected based on evolutionary distances. Similar techniques will apply to the isolation of the genomic sequences that encode ALF and SALF, as well as those that encode related genes from organisms other than humans. Reference is particularly made to flanking regions, including upstream sequences that encode the core promoter and regulatory regions, as well as downstream regions, introns and intron/exon boundaries. Similar techniques will also apply to the identification of mutant alleles, polymorphisms, deletions, insertions, and so forth, in genomic and cDNA sequences. These may occur within the ALF and SALF sequences themselves, or may occur in regulatory regions, introns, intron/exon boundaries, or may reflect various insertions, partial or whole gene deletions, or substitutions, any of which may affect biological activity of a gene and gene product. In the case of humans, the identification of interindividual genomic differences in the ALF and SALF genes will be useful in diagnostic determinations.

Whole or partial sequences referred to above may also be identified and isolated using techniques that involve annealing of short oligonucleotides to complementary sequences, such as those as might be present in the genomic DNA of a particular organism, or in genomic or cDNA, including expression cDNA, libraries. Thus, PCR is used to obtain DNA sequences homologous to, and which lie between, two primers, usually between 15 to 30 nucleotides which have annealing temperatures typically between 60-80 degrees Celsius may be substantially purified. The choice of primer sequences, annealing conditions (temperature), number of amplification cycles, choice of polymerase, and so forth would be within the knowledge of one skilled in the art. Amplification assays will be generally applicable to the identification of sequences homologous to ALF and SALF, to the identification of flanking genomic or cDNA sequences, to the identification of mutated alleles, and so forth, in a manner that lends itself to rapid diagnostics.

Variations in PCR technology are also relevant, such as reverse transcriptase mediated PCR, in which mRNA or total RNA is reverse transcribed typically with an oligo dT or gene specific primer prior to PCR amplification. Techniques are also available which utilize only one gene-specific primer, together with a linker or adapter primer as may be present in a vector or attached to the ends of the DNAs to be amplified. For instance, the
5 Genome Walker (Clontech) technique allows the isolation of genomic DNA that flanks a given oligonucleotide primer. Thus, the invention provides a method to isolate the testis-specific ALF gene promoter that can be used to drive cell- or tissue-specific expression of unrelated genes. Techniques are also available in which altered oligonucleotides are employed to generate specific mutations, deletions, insertions, or fusions in the disclosed
10 sequences, or fragments thereof, for instance site directed mutagenesis.

Likewise, the current invention provides methods to map particular regions of a chromosome, and to identify and isolate homologous regions in artificial chromosomes, such as YACs, PACs, single chromosome libraries, and so forth. The current invention also
15 provides techniques such as *in situ* hybridization in order to map disease-associated genes or other chromosomal markers, as well as mutations such as polymorphisms, inversion, translocations, deletions, insertions, and the like, which may be associated with particular health conditions.

Naturally, it will be understood that this invention is not limited to the particular
20 nucleic acid sequences presented herein. Recombinant vectors, including for example plasmids, phage, viruses, and other sequences, and isolated DNA or RNA segments may therefore variously include the ALF and SALF sequences or their complements, and coding regions, as well as those that may bear selected alterations or modifications that nevertheless include ALF or SALF segments or may encode biologically or experimentally relevant amino
25 acid sequences. Such sequences may be created by the application of recombinant DNA technology, where changes are engineered based on the consideration of the nucleotides or amino acids being exchanged, deleted, inserted, fused, or otherwise modified.

Likewise, the current invention encompasses sequences that may be naturally present as extensions of, or insertions within, the sequences disclosed herein, including alternative

or longer 5' or 3' mRNA sequences, or intronic and promoter genomic sequences, or allelic or polymorphic versions of a gene. Similarly, natural, artificial, or synthetic fusions of ALF and SALF, and fragments thereof, with unrelated nucleic acids or amino acids such as those that encode epitope tags, binding proteins, marker proteins, and other amino acid sequences
5 are included.

ALF AND SALF PROTEINS AND POLYPEPTIDES

One aspect of the invention is the protein, polypeptide, oligopeptide, or amino acid sequences or fragments thereof, of ALF and SALF, essentially as set forth in SEQ ID NOS.
10 2, 4 and 6. Sequences that have greater than about 40-50% homology with any portion of the amino acid sequences described herein, sequences that have between about 51% and about 60%; sequences that have between about 61% and about 70% sequences that have between about 70 and about 80%; or between about 81% and about 90%; or between 91% and about 99%; or those that contain amino acids that are identical, functionally equivalent,
15 or functionally irrelevant, for instance those specified by conservative, evolutionarily conserved, and degenerate substitutions, with respect to the amino acid sequences presented in SEQ ID NOS 2, 4 and 6 are included. The invention thus applies to ALF and SALF sequences, or fragments thereof, and nucleic acids which encode such polypeptides, such as those of other species. Reference is particularly, but not exclusively, made to the conserved
20 N- (amino acids 1-54) and C-terminal (amino acids 417-478) regions of ALF and SALF, in contrast to similarity throughout the entire length. The invention thus encompasses amino acid sequences, or amino acid-like molecules, that are sufficient in any regard to mimic, substitute for, or interfere with the ALF or SALF amino acid sequences, or fragments thereof.

The invention encompasses ALF and SALF amino acid sequences that have been
25 altered in any form, either through the use of recombinant engineering, or through post-translational or chemical modifications, including those that may be produced by natural, biological, artificial, or chemical methods. Naturally, it will be understood that this invention is not limited to the particular amino acid sequences presented herein. Altered amino acid sequences include those which have been created by the application of

recombinant technology such that specific residues, regions, or domains have been altered, and which may be functionally identical, or which may possess unique biological or experimental properties with regards to function or interactions with natural and artificial ligands.

For instance such modifications may confer longer or shorter half-life, reduced or increased sensitivity to ligands that modify function, ability to detect or purify polypeptides, solubility, and so forth. Alternatively, such sequences may be shorter oligopeptides that possess an antigenic determinant, or property that interferes, or competes, with the function of a larger polypeptide, for instance sequences similar to the functionally important and conserved N- and C-terminal domains, and those that affect interactions between TFIIA subunits and other proteins. Such sequences may be created by the application of recombinant DNA technology, where changes are engineered based on the consideration of the nucleotides or amino acids being exchanged, deleted, inserted, fused, or otherwise modified. Likewise, the current invention encompasses sequences that may be naturally present as extensions of, or insertions within, the sequences disclosed herein, including alternative or longer N- and C-terminal sequences, or alternatively spliced protein isoforms.

Production and purification of polypeptides may be achieved in any of a variety of expression systems known to those skilled in the art, including recombinant DNA techniques, genetic recombination, and chemical synthesis. For instance, expression in prokaryotic cells may be achieved by placing protein coding nucleic acid sequences downstream of a promoter, such as T7, T3, lacI, lacZ, trp, or other cellular, viral, or artificially modified promoters including those that may be inducible by IPTG, tetracycline, maltose, and so forth. Such promoters are often provided for in commercially available recombinant DNA vectors such as pRSET ABC, pBluescript, pKK223-3, and others, or are easily constructed to achieve such a purpose, and often include the presence of multiple cloning sites (MCS) to facilitate restriction digestion mediated cloning of full or partial coding fragments. Such vectors typically contain efficient ribosome binding sites, and in some cases transcription termination signals.

Cells for the expression of such proteins are normally *E. coli*, but could include *B. subtilis*, *Streptomyces* or others prokaryotes. The incorporation of such recombinant DNA can be efficiently achieved by calcium chloride transformation, electroporation, and so forth. In the case of *E. coli*, cells typically grow in LB media with an appropriate antibiotic selection, for instance ampicillin, chloramphenicol, tetracycline and so forth in order to retain the recombinant vector, although vectors which integrate into the cellular chromosome are also possible. The promoter of many recombinant expression vectors require induction by an inducer compound, for instance IPTG, to facilitate high levels of transcription initiation and subsequent protein production. In some instances, nucleic acid sequences within the coding region may be altered to suit the codon usage patterns of a given model expression system or organism.

Peptides, oligopeptides and polypeptides may also be produced by chemical synthesis, for instance solid phase techniques, either manually or under automated control such as Applied Biosystems 431 peptide synthesizer (Perkin Elmer). After synthesis, such molecules are often further purified by preparative high performance liquid chromatography. Thus, the invention provides methods for the production of epitopes for antibody production, or the production of small molecules that enhance or interfere with a specific function or interaction of the ALF or SALF polypeptides.

Methods to produce and purify said polypeptides in eukaryotic systems are widely available and understood by those proficient in the art. Cells for such production are known to include yeast and other fungi, Drosophila and Sf9 cells, cells of other higher eukaryotic organisms such as HeLa, COS, CHO and others, as well as plant cells. Similarly, expression could be achieved in prokaryotic or eukaryotic extracts that are able to translate RNAs into proteins, such as rabbit reticulocyte lysates.

Vectors for expression in such systems are widely available both commercially or can be prepared. Such vectors typically are driven by promoters derived from cellular or viral genes, such as CMV, HSV, EBV, SV40, Adenovirus, LTRs, vaccinia, baculovirus polyhedrin promoter, CaMV, TMV, Rubisco, and so forth, and could obviously include the promoters for the ALF or SALF genes themselves. Such vectors are often designed to

regulated by the presence of enhancer or other regulatory element sequences. Introduction of such vectors into cells is often achieved by calcium phosphate or DEAE dextran technologies, liposome mediated techniques, electroporation, or viral mediated infection. Maintenance of such vectors may be achieved by selectable marker such as that conferred by HSV thymidine kinase, HGprtase, herbicide resistance, visible markers, and so forth.

Selection of an appropriate methodology would be within the scope of those skilled in such methodologies, using the current invention, and would include any combination of host cell and vector which can achieve desired production goals. For instance, the ability of a host cell to drive efficient full-length polypeptide production, glycosylation, membrane anchoring, secretion, absence of contaminating mammalian proteins or infectious agents, proteolytic processing, lipid modification, phosphorylation and so forth may dictate the use of baculovirus/insect cell systems, mammalian cells systems, plant cell systems and so on. In the case of in vitro translation extracts, one embodiment is the coupled transcription and translation of a nonreplicable recombinant vector, where translation is often visualized by the incorporation of a radiolabeled amino acid. The system selected may further depend on the desirability of obtaining purified polypeptides for further characterization, on whether the intent is to evaluate the effect of the overexpressed proteins on cellular gene expression, in vivo or in vitro, to identify compounds that enhance or interfere with the function of the overexpressed polypeptides, or other purposes.

For stable, long term expression, integration within the host cell chromosome, or as an autonomously replicating element, may be used. ALF or SALF genes, including defective (knock-out) genes themselves, can also be introduced to produce transgenic animals, for instance rodents, primates, insects, and other organisms. These methods provide an opportunity to develop and study animal models for specific gene defects, or for augmented expression of certain genes. Such techniques include pronuclear microinjection, retrovirus mediated transfer and other viral vectors, gene targeting into embryonic stem cells, homologous or nonhomologous recombination and electroporation. The presence and expression of transgenes may occur in all or some cells of a given organism. Likewise, expression of the transgene may be constitutive or inducible and may occur in all or only

some cell types. Characterization of the introduced transgene, or mutant (knock-out) construct is typically achieved by genomic Southern blotting and/or PCR analysis of genomic DNA, and its expression by RNA-RNA, DNA-RNA, DNA-DNA hybridization such as Northern analysis, or by RT-PCR analysis.

5 The invention also relates to cells which contain such recombinant constructs, where the host cell refers to mammalian, plant, yeast, insect, or other eukaryotic cells, or to prokaryotic, or archae, and vectors that are designed for a given host. Promoter-vector combinations could be chosen by a person skilled in these arts. In some cases, the desired outcome may not be protein, but RNA, and recombinant vectors would include those with 10 inserts present in either forward or reverse orientations.

15 Many of the vectors and hosts have specific features that facilitate expression or subsequent purification. For instance DNA sequences to be expressed as proteins often appear as fusion with unrelated sequences that encode polyhistidine tags, or HA, FLAG, myc and other epitope tags for immunochemical purification and detection, or phosphorylation sites, or protease recognition sites, or additional protein domains such as glutathione S-transferase (GST), maltose binding protein (MBP), and so forth which facilitate 20 purification. Vectors may also be designed which contain elements for polyadenylation, splicing and termination, such that incorporation of naturally occurring genomic DNA sequences that contain introns and exons can be produced and processed, or such that unrelated introns and other regulatory signals require RNA processing prior to production of mature, translatable RNAs. Proteins produced in the systems described above could be subject to a variety of post-translational modifications, such as glycosylation, phosphorylation, nonspecific or specific proteolysis or processing.

25 Purification of ALF, SALF, or carboxy terminal variants produces as described above can be achieved by any of several widely available methods. Cells may be subject to freeze-thaw cycles or sonication to achieve disruption, or may be fractionated into subcellular components such as nuclear and cytoplasmic fractions prior to further purification. Purification may be achieved by one or more techniques such as precipitation with salts or organic solvents, ion exchange, hydrophobic interaction, HPLC and FPLC chromatographic

techniques. Affinity chromatographic techniques could include the use of polyclonal or monoclonal antibodies raised against the expressed polypeptide, or antibodies raised against or available for an epitope tag such as HA or FLAG. Similarly, purification can be aided by affinity chromatography using fusions to the desired proteins such as GSH-affinity resin, maltose affinity resin, carbohydrate (lectin) affinity resin or, in a one embodiment, Ni-affinity resin, and so forth. In some instances purification is achieved in the presence of denaturing agents such as urea or guanidine, and subsequent dialysis techniques may be required to restore functionality, if desired.

10

ANTIBODIES TO ALF AND SALF PROTEINS

The current invention encompasses antibodies of any class, such as IgA, IgD, IgE, IgG, IgM, and subclasses, including polyclonal, monoclonal, chimeric, single chain, humanized and antibody fragments, including synthetic antibodies as in recombinant antibody expression library, single chain antibodies, anti-idiotype antibodies and other immunological, or binding, factors that recognize one or more epitopes of the ALF and SALF proteins. Such reagents as derived from ALF and SALF provide methods for detection and purification of ALF and SALF polypeptides, including endogenous, recombinant, or synthetic factors, and as a means to affect changes in gene expression or other functions by immunochemically targeting ALF or SALF. Proteins, polypeptides, oligopeptides, or peptides will be suitable for the production of monoclonal and/or polyclonal antibodies against the ALF, SALF, and alternative C-terminal regions, and for the use as standards or controls in assays such as ELISA, RIA, FACS, Western analysis, and so forth.

Antigens used to generate antibody reagents have a length of at least five amino acids, and in some cases 10 or more, up to the length of the full-length protein. Techniques that are used to obtain such reagents are described in, e.g., Harlow, et al., *Antibodies: A laboratory Manual*, Cold Spring Harbor Laboratories, New York (1988). For polyclonal antibodies, animals such as rabbits, mice, rats, goats, and so forth are injected with up to several hundred micrograms of antigen together with an adjuvant such as Freund's, either complete or incomplete, followed by a series of booster injections. Blood (serum) collected at intervals

following injections are tested for antibody titer and specificity. Use of such antibodies is often facilitated by further purification by salt fractionation, antigen affinity chromatography, or other purification methods, to obtain more pure, and thus more specific, antibodies.

Monoclonal antibody production can be achieved by several methods, including the hybridoma technique, the human B-cell hybridoma technique and the EBV-mediated hybridoma technique. Thus, in one embodiment, antibody producing cells from mice spleen are fused with myeloma cells. Hybrids are then subcloned and screened for antibodies with the antigen, in this case ALF, SALF, the alternative C-terminal domain, or related antigenic fragments. Antibodies against related polypeptides which are intended for the same purpose constitute an included methodology for detection.

Humanized antibodies are those in which the antigen recognition region from an antibody with a given specificity that possess domains from human antibodies so as not to be recognized or rejected by humans. Chimeric antibodies are those in which genes for the antigen recognition region and the constant regions are spliced from different organisms, for instance mouse and human.

In another embodiment, ALF or SALF antigens may be used to generate an immunological reaction, as described above, which generates an immunological response that, in turn, causes a biological or developmental effect, such as modulation of gene expression, or which affects a cellular process such as testis function or spermatogenesis.

DETECTION OR DIAGNOSIS OF ALF OR SALF GENES, GENE PRODUCTS AND ABNORMALITIES THEREOF.

One embodiment of the invention is the use of the invention for the detection of DNA and RNA sequences of ALF, SALF and the alternative carboxy terminus. Such efforts might be directed towards evaluating the levels of these polynucleotides, to evaluate whether such sequences are present or absent in given individuals, or to evaluate whether corresponding sequences in given individuals are in some way absent, abnormal, or otherwise altered. Thus, the invention encompasses methods and reagents for the production and use of oligonucleotide probes, or DNA or RNA probes of various lengths, that have sufficient

similarity to ALF and SALF nucleic acids to allow for selective detection. Methods for labeling could employ radioactive nucleotides, e.g., using T4 polynucleotide kinase, DNA polymerases, in vitro synthesis of RNA probes, PCR amplification of labeled DNAs, as well as nonradioactive techniques such as incorporation and detection of fluorescent, chromogenic, chemiluminescent compounds, as well as avidin/biotin based systems.

Other detection methods could include those based on direct hybridization, such as include fluorescent in situ hybridization (FISH), in situ hybridization, DNA "chip", or "microarray" hybridization technology, Southern and Northern hybridization analysis, RNA dot blot hybridization, dipstick, pin, dot blot, in situ PCR, and other techniques. Others methods may be based on annealing between short, typically 15-30 nucleotide, complementary DNA or RNAs followed by enzymatic extension, such as PCR analysis of genomic DNA or cDNA, reverse-transcriptase mediated PCR using RNA. Such oligonucleotides are derived from the sequences in SEQ ID NOS 1, 3, or 5, or their complements, or from flanking 5'- or 3' cDNA or genomic regions, or from introns or alternatively spliced exons, alleles, promoter or enhancer regions, and so forth. Visualization of the results from such methods is accomplished by a number of methods, including light or fluorescent microscopy, autoradiographic detection, or detection based on ethidium bromide stained agarose gels, DNA sequencing, and so forth. These and other techniques would be those available to and recognized by those skilled in the art.

To provide a basis to establish whether gene structure or expression correlates with a given pathology, results between normal and experimental subjects are compared with respect to the sizes of hybridizing bands, nucleic acid sequence differences, quantitative differences in gene copy number and expression. Thus standard values from normal individuals are compared to those from individuals which display a particular set of symptoms to determine if symptomatic individuals fall outside normal deviations. Such detection may be facilitated by ELISA, or microplate, type assays in which a chemical composition may be coupled to a support to facilitate reading of multiple samples rapidly, for instance in an automated format, as judged by some spectrophotometric or colorimetric response. Such techniques could also be used to assess the efficacy of other treatments

related to the function or production of ALF or SALF genes and gene products. The ability to detect corresponding DNA or RNA sequences could be provided for in an appropriately licensed pharmaceutical kit that would contain sequence-specific reagents capable of selective detection. Such detection might be made with whole genomic DNA, for example from blood or other tissues, or from RNA or DNA obtained from cultured cells or sampled tissues, or using chromosomes of cells, as examples.

Comparison among samples derived from given individuals using a given detection methodology, for example differential hybridization, conformational polymorphisms, sequencing, and so forth would be compared to those from normal controls. Such procedures may be directed towards the detection of ALF, SALF, and alternative carboxy terminal sequences themselves, or to corresponding genomic sequences, including the promoter and intronic sequences, or to the lack of these sequences due to deletion. Detection procedures would enable differences in test samples, for example those which may be testis-derived, including those which may be dysfunctional or cancerous, to be compared with normal samples.

In one embodiment of the invention, a polynucleotide sequence derived from those disclosed herein is used as a target in a microarray as a means to identify the presence or absence of expression, the presence or absence of gene mutants, and so forth. For instance, an oligonucleotide, or oligonucleotides, are synthesized (typically between 6 and 70 or 80 nucleotides long) that are computer optimized for minimal secondary structure and minimal likelihood of nonspecific interactions. These oligonucleotides, or mixed sets of oligonucleotides, are then coupled to, or synthesized directly on a support, usually in a grid arrangement, such as nylon, glass, or other membrane, wafer, chip, slide, and so forth. Labeled probes from a biological sample may be either DNA, RNA, or reverse transcribed DNA, are used to hybridize to the microarray. After washing, the retention of the probe to a given oligonucleotide is typically determined by fluorescence analysis in a scanner. These techniques are understood by one of skill in the art and performed in accordance with the appropriate instrumentation.

Alternatively, the invention provides a method for isolating identical or related genes from humans or other organisms that may have similar functionality, for instance by PCR or hybridization analysis of genomic and/or cDNA libraries. The invention also provides a means to identify the corresponding genomic DNA and the corresponding tissue-specific promoter DNA and regulatory sequences.

The present invention provides a means to use the ALF or SALL specific antibodies described above in the form of an appropriately licensed kit or pharmaceutical pack which contains reagents and supplies for detecting the expression of relevant polypeptides in cells and tissues. Such approaches include enzyme-linked immunosorbent assay (ELISA),
10 radioimmunoassay (RIA), fluorescent activated cell sorting (FACS). Another approach is a Western blot, in which crude protein extracts are separated on SDS-PAGE gels, transferred to nitrocellulose and hybridized with a specific antibody. Hybridization typically involves prior blocking with nonspecific proteins and dilution of antibody to a level that facilitates specific as opposed to nonspecific interactions. Visualization typically occurs by the action
15 of a secondary antibody which is typically coupled with a domain such as horse radish peroxidase or radiolabeled protein A which possesses an activity or property which can be visualized. Samples tested may be identical in size and abundance to those observed in normal samples, or they may be increased or decreased in abundance, or they may possess altered mobilities.

Likewise, the level of ALF and SALL antigen in a given sample may be evaluated through the use of an ELISA assay, in which samples are attached to a support, typically a set of plastic wells and are incubated with specific antibody. After washing, secondary antibodies are added that allow visualization, and indicate levels, of the primary antigen which are present. Controls, or standards, would consist of recombinant antigen present in
20 a series of dilutions, as a standard curve. Plates are then read with a microplate spectrophotometer. Antibodies are also used for immunolocalization of antigenic proteins within tissues and cells, to determine appropriate expression and localization of antigen among various subcellular compartments. Antibodies may be employed in specific immunoprecipitation or immunopurification protocols that are designed to identify and
25

isolate corresponding cellular antigens, or complexes that may contain such antigens. Differences among cells or tissues that may be causative with respect to abnormal biological function are identified in this way.

The invention also provides a means to identify endogenous levels of ALF and SALF activity. Tissue samples or biopsies are obtained and extracts of nuclear proteins or whole cell extracts are produced by homogenization in a physiological buffer together the presence of protease inhibitors, if necessary. Extracts are then tested directly for activity, for instance as described in the TBP-dependent bandshift assay. Alternatively, further precipitation or chromatographic purification may sometimes be necessary to isolate and differentiate endogenous activities away from crude samples.

IDENTIFICATION OF LIGANDS AND INTERACTION PARTNERS OF ALF AND SALF

The invention provides a method of identifying compounds, whether they be specific chemicals or drugs, polypeptide fragments of ALF, SALF or other proteins, in vitro or in vivo selected oligopeptides isolated by selections such as phage display, or RNA or DNA sequences that with affinity for such proteins and complexes. Such compounds are typically identified based on affinity-based interaction assays, or on their ability to modulate function in simple representative functional assays, for instance, modulation of TBP-TATA interactions as visualized by bandshift assays. Such compounds are typically next tested in an in vitro functional assay such as that described to test their ability to interfere with (antagonists), or facilitate (agonists), the function of RNA polymerase II, either in terms of basal or activated transcription. Such compounds may be tested in tissue-derived cells, or in cell lines for modulation of activity, for instance gene expression. Such compounds are then evaluated for their efficacy as therapeutic agents, particularly with respect to the modulation of gene expression in a tissue or organisms itself.

Thus, such compounds may be added individually, or in pools, to assess whether in the presence of the polypeptides, RNA polymerase II and other required general factors and upstream activators, and they can affect initiation and chain elongation of RNA from

particular promoters, including those which may be tissue- or cell-type specific. For instance, compounds may be tested for their ability to modulate the expression of genes that require ALF or SALF function, as judged by visualization of a reporter such as beta-galactosidase, luciferase, G-free cassette, and so forth. Similarly, the invention provides
5 a method to identify compounds that could confer could confer an activated phenotype, or a dominant negative phenotype, in terms of the polypeptides themselves. In particular, mutations are constructed according to site-directed mutagenesis techniques or by random mutagenesis techniques that are known to practitioners of the art, and selected and evaluated for functionality. Further, computer modeling of the ALF or SALF polypeptides, either
10 based on X-ray crystallographic data, or on comparisons with known TFIIA structures provides a method to fit, or design, compounds that may interfere with various functions or interactions of ALF or SALF, for instance subunit- subunit interactions, subunit-TBP interactions, and so forth.

The method also provides for solid phase high throughput screening methods for
15 identifying ligands which interact with ALF or SALF. For instance ALF or SALF, alone or with a TFIIA γ subunit, or even with TBP, promoter DNA, or other factors, are linked to a solid support. Compounds to be tested for interaction are co-incubated, washed to remove nonspecific or less specific interactions, and those that remain are of relatively higher affinity. Detection is achieved by any of a number of techniques, including antibody linked
20 markers, radioisotopic counting and so forth, preferably via automated sample handling.

Identification of ligands may also be achieved using multiple rounds of PCR-mediated selection of high affinity nucleic acid ligands, in which interacting ligands are typically separated from non-interacting ligands by gel shift. Likewise, the promoter element sequences that have affinity for ALF or SALF containing complexes, for instance those
25 which contain TFIIA γ and even TBP, can be selected for by multiple rounds of PCR amplification starting from either random or TATA-containing oligonucleotides. The derived sequences may be compared to the genomic DNA sequences, such as promoters.

Factors such a proteins, or small peptides that interact with ALF or SALF may be identified by phage display, in which a library of oligopeptides with diverse sequences are

detected by virtue of their ability to be recognized, or selectively retained by, ALF or SALF polypeptides that are labeled, or fixed to solid support. Interacting phage are detected, reamplified and reselected until single isolates, or plaques are obtained. The sequence of the interacting motif is identified by sequencing all or part of the coat protein which has been engineered to contain such sequences.

The invention also provides techniques to identify natural interacting proteins of ALF and SALF. For instance, immunoprecipitation using antibodies specific to ALF, or SALF, or to epitope tags that have been engineered within recombinant ALF or SALF nucleic acids, can be used to remove, or pull-down, ALF and SALF containing complexes from cellular extracts, for instance those derived from testis tissue or testis cell lines. Such techniques can be performed either in solution, or with the antibody linked to a solid support, such as a resin or a well.

Similarly, ALF or SALF with GST-encoding nucleic acids in the form of a recombinant expression vector allow overproduction and purification of the fusion protein. Such a protein may be bound to affinity resin such as S-hexyl glutathione, and cellular or recombinant proteins, or fragments thereof, can be tested for their ability to interact with ALF or SALF. Such an analysis typically involves comparisons of the bound proteins compared to eluted proteins using a resin that is loaded with the fusion protein and a resin that is loaded with the GST domain alone.

The yeast two-hybrid and related systems also provide methods to identify interacting factors. In this method, genetic fusions of DNA binding domains and activation domains are made separately to the target and bait polypeptides and clones that express interacting epitopes are identified based on a transcription activation assay *in vivo*. This may be performed in variety of cell types, including yeast and mammalian cells.

The invention provides a means to identify genes which may be selectively regulated by the ALF or SALF polypeptides. For instance, targets of ALF or SALF function may be identified in cells which are engineered to overexpress, or underexpress the ALF or SALF genes, or altered forms of these proteins. RNA isolated from such cells may be purified and compared to that present in normal cells. For instance, differential display, subtractive

hybridization and microarray techniques are available to evaluate differences in gene expression, or RNAs, present in two or more populations. For use with microarray analysis, gene specific oligonucleotides or segments, typically 6 to 70 or 80 nucleotides are coupled to, or synthesized on, a solid support and mRNA populations (cDNA) are prepared from normal control cells or tissues and from cells or tissues which are either overexpressing ALF or SALF, or which contain knockouts in these genes. After hybridization and washing, the microarrays can be scanned for hybridization, for instance as registered by fluorescence. In this way genes whose expression is unaltered, decreased, or increased in response to the presence or absence of the transcription factors ALF or SALF can be identified.

Likewise, serial analysis of gene expression (SAGE) analysis provides a method in which short sequences derived from cDNAs from two populations of mRNA are quantitatively compared for their frequency of identification. The technique relies on the use of restriction enzymes that cut away from their binding site and the concatamerization of the resulting fragments into a vector for sequencing. Thus, single sequencing runs of each isolate can give data from multiple original cDNAs. Confirmation of the isolates is often achieved by Northern or quantitative or semi-quantitative PCR analysis. Thus, engineered ALF and SALF genes provide a method to identify additional genes that are "downstream" or regulated, by ALF or SALF, which may in turn be targets for detection, diagnosis and intervention with regard to correlating disease conditions.

TREATMENT OF ALF- AND SALF-RELATED DISORDERS

The invention provides methods for the isolation, detection, diagnosis, development of animal models, or therapeutic protocols applicable to any organism, such as cats, dogs, pigs, cows, horses, rabbits, birds, primates and humans. Thus, nucleic acid sequences, antibodies and other agonistic or antagonistic ligands may be used to inhibit or augment patterns of gene expression by modifying ALF and SALF function, or the function of the ALF or SALF genes themselves. Such compounds could be delivered in various media, including buffered saline or other carriers or solvents dependent on the chemical nature of the compound and the route of delivery. Delivery mechanisms could include intranasal,

subcutaneous, intramuscular, intraperitoneal, intradermal, intravenous, topical, enteral, rectal, intramedullary, intraarterial, sublingual, or other means. Doses would vary depending on the need to alleviate or correct particular symptoms and on the particular agent. Standard measures of effectiveness and toxicity in cell cultures and animals are given by ED₅₀, the dose that is therapeutic for 50% of the sample, and LD₅₀, the dose that is lethal to 50% of the sample. Administration of polypeptides, drugs and other therapeutic compounds would be apparent to those skilled in the art with respect to the present teachings, and in accordance with licensing and regulatory requirements. Normal dosages range from 0.1 ug to 100 mg, up to a total dose of 1g, depending on the particular formulation, delivery route, patient sensitivity, patient history, clearance rates, half-life, and other considerations as would be generally available to one skilled in the art. Compositions with high therapeutic indices will generally be used. Additional details are available in such references as Remington's Pharmaceutical Sciences. Initial estimates as to effective concentrations may be determined using cells grown in culture, or in animal models. The invention also provides for the use of proteins, agonists, antagonists, nucleic acid sequences and vectors administered in conjunction with other therapeutic agents, according to accepted usages by those skilled in the art.

Concentrations for delivery of nucleic acids, polypeptides, antibodies and transgenics will be specific to particular cells, conditions, etc. For instance, the invention provides methods for the use of oligonucleotides, phosphorothioate oligonucleotides, peptide nucleic acids and other nucleic acid-like, or nucleic acid binding molecules that could be administered in a manner and amount designed to treat the specific indications using antisense therapy. Such sequences may contain additional, or other modifications, such as methylation, acetylation, thiolation of normal bases, as well as the use of unconventional bases in order to enhance stability. Such complementary sequences are generally targeted along the coding or control regions of ALF or SALF, so as to control transcription or translation and may be supplied as a drug, or as an antisense transcript, or other functional molecule such as a ribozyme, derived from a transgene.

Similarly, pharmaceutical intervention would also be applicable to specific antibodies and to other compounds that target ALF and SALF function. Therapeutic antibodies that recognize ALF or SALF may be used to directly target, and inactivate, ALF and SALF polypeptides through antibody-epitope interactions, possibly when coupled with compounds that facilitate cellular entry. Likewise, such antibodies may serve as a carrier or targeting molecule by which other therapeutic compounds might be brought to cells which harbor ALF or SALF.

ENGINEERED ORGANISMS AND ANIMAL MODELS

The present invention provides methods for the production of engineered cells and organisms such as rodents, but which may include humans or other organisms in need of therapy, that express ALF or SALF or altered forms in the form of a recombinantly introduced gene (transgene). For instance, cells can be engineered with polynucleotide sequences so that expression of active or dominant negative ALF or SALF polypeptides are produced, for instance to compensate for the loss, or overactivity, of such polypeptides in a patient. The current invention also provides methods for ex vivo gene therapy, in which recombinant vectors are introduced into stem cells, or other accessible cell population, and, after engineering and propagation, are transplanted back into the patient. Such engineered constructs might be designed to produce RNA that will be translated into ALF or SALF proteins, or altered versions thereof. Alternatively, such constructs might be designed to produce antisense RNA designed to inhibit transcription or translation, or to produce ribozymes that target ALF and SALF RNAs for degradation. Alternatively, the current invention also provides methods by which deletions, or knock-outs of the ALF or SALF genes can be produced, in order to establish animal models for pathological conditions that result from the absence of these genes.

These methods are known to those in the art, and may include stable integration of DNA sequences by recombination, adenoviral, retroviral and other means which are intended to introduce and propagate sequences in engineered cells, by techniques such as pronuclear microinjection, liposome mediated uptake, electroporation of embryos, homologous

(targeted) recombination, and so forth. One embodiment is receptor-mediated gene transfer, whereby the transgene is coupled with a ligand via polylysine, where the ligand is some molecule that interacts selectively with surface molecules, or receptors, on a selective cell population such as those that might be present in testis, or an antibody that has specificity for
5 a cell-specific surface marker.

Depending on the method chosen, the introduced gene might replicate autonomously as part of a vector, or may integrate a specific or random sites. Such a gene may be engineered so as to contain regulatory sequences that drive expression in a constitutive, inducible, tissue- or cell-cycle specific, or other manner, as desired. Another embodiment
10 of the invention is the use of homologous recombination targeting vector that contains a recombinant ALF or SALF gene that has been engineered to be nonfunctional. Such a construct can be used replace the endogenous gene by homologous recombination, for instance, in embryonic stem ES cells from mice, followed by selection, implantation and development of the modified cells into adult organisms which contain targeted defects in
15 ALF or SALF genes.

The presence of the transgene, or knockout construct, may be established by genomic blotting or genomic PCR, and its expression, or lack thereof, by Northern blotting or RT-PCR, or other hybridization technologies. Transgenes that express ALF or SALF proteins, or altered forms, can be further detected using antibodies specific for the expressed protein. Once transgenic founder animals are produced, they are bred to produce colonies
20 of animals with particular genotypes, including inbreeding and outbreeding to develop homo- and heterozygous animals, with respect to the transgene, in different backgrounds. Cells derived from such animals may also be isolated and propagated for study. Further examination at the organismal, tissue, cellular, subcellular and biochemical levels will
25 establish the biological effects of organisms that contain engineered ALF or SALF genes. Such organisms and cells will also provide assay systems with which to identify agonists and antagonists that may compensate for observed defects, and which may perform similar functions in other organisms, including humans.

The invention may be better understood with reference to the following examples. These examples, however, should not be taken to limit the scope of the invention in any way.

EXAMPLE 1

CLONING AND DETECTION OF ALF AND SALF

The 5'-end of SALF was amplified by PCR (40 cycles) using 4 µl of the human placental cDNA library (Clontech) with primer 2a2-6 (5'-AGTAACCCGAATGCTTAA- 3') (SEQ ID NO.: 8) and a commercially available library-specific adapter primer AP1 (Clontech). The resulting products were reamplified (35 cycles) with primer 2a2-8 (5'ATGCTAGCTGAACCACTG-3') (SEQ ID NO.: 9) and a commercially available nested library-specific adaptor primer AP2 (Clontech) used to obtain a 2,930 bp product, which was subcloned into the pCRII cloning vector (Invitrogen) to form pRACE4 (FIG 7A). Sequence analysis of this and EST ID 256637 constitute SEQ ID NO. 3. Human SALF cDNAs were identified by PCR amplification (35 cycles) of 1.1 and 0.9 kb products from human placenta, liver and testis "Marathon" cDNA libraries (Clontech) using 25 pmol of the upstream primer 2a2-1 (5'- AGAAATTCCCTCTGATTG-3') (SEQ ID NO.: 7) and the downstream primers 2a2-6 and 2a2-8. The 1.1 and 0.9 kb products derived from the liver cDNA library were subcloned into pGEM-T Easy (Promega). Sequence analysis of the liver-derived products shows that they are identical to those present in both SEQ ID NO. 3. These products are diagrammed in FIG 7A, and shown in FIG 7C.

ALF sequences were isolated by PCR (35 cycles) using 4 µl of the human testis cDNA library (Clontech) with the gene-specific primer 2a2-20 (5'-CCAGAACGGTAGAATTGCGGGTTGCTGTAGC-3') (SEQ ID NO. 12) and primer AP1 (Clontech), and reamplified with 2a2-22 (5'-GGAGTTGAAGTGCCCAGGTCTGCTGTGG-3') (SEQ ID NO.: 19) and primer AP2 (Clontech). The 369 bp amplification product is subcloned into pGEM-T Easy (Promega) to form pRACE22. The resulting clone (pRACE22; FIG 7B) contains 298 bp that are identical to SALF and a 35 bp 5'-end that is unique to SEQ ID NO. 1. A full-length ALF PCR product is amplified (35 cycles) from 4 ml of the testis cDNA library (Clontech) using

primer 2a2-17 (5'- GGTGCTGTCATGGCCTGCCTCAACCCGG-3') (SEQ ID NO. 13), located within the unique 5'-end of ALF, and primer AP1 (Clontech). The resulting 1.7 bp fragment is subcloned into pGEM-T Easy to form pRACE17 (FIG 7B). The sequence of the resulting clone is identical to the composite SALF sequence except for its unique 5'-end and a longer poly(A) tail (~90 nucleotides) which begins four nucleotides downstream of the poly(A) tail in SALF. The composite sequences of pRACE17 and pRACE22 are SEQ ID NO. 1.

EXAMPLE 2

DETECTION OF GENOMIC DNA SEQUENCES THAT ENCODE ALF.

Genomic DNA (10 µg) from HeLa cells is digested with the indicated restriction enzymes (BglII and EcoRI), electrophoresed on 0.7% agarose gels using 1X TBE buffer, and transferred overnight to nitrocellulose membranes (Schleicher and Schuell). Hybridization is performed under stringent conditions at 42° C in 50% formamide, or at 68° C, in hybridization buffer (6X SSC, 0.5% SDS, 5X Denhardt's solution, and 100 µg/ml salmon sperm DNA). The probe is a full-length NdeI-BamHI ALF fragment contained within the vector construct pRSET-ALF. The blot is washed at 65° C in 0.1X SSC and 0.5% SDS, and exposed at -80° C to XAR-5 film (Kodak). Hybridization with the ALF probe revealed bands of 8.6, 6.9, 5.0, and 1.0 kb (BglII; lane 1), or 11.5, 8.4, 6.0, and 4.5 kb (EcoRI; lane 2). These results (FIG 9) show that sequences complementary to ALF are present and detectable in human genomic DNA.

EXAMPLE 3

EXPRESSION OF ALF AND OTHER HUMAN TFIIA SUBUNIT mRNAs

Northern blots containing 2 µg of poly(A) mRNA from 16 human tissues are obtained from Clontech. Gene-specific probes for hybridization are as follows: ALF, a 621 bp NcoI-KpnI fragment or an 899 bp HincII-BglII fragment from region II (FIG 7B); 5'-SALF, a 1,002 bp EcoRI-EcoRI fragment from pRACE4 containing the 5'-UTR and nucleotides

encoding the first 282 residues (FIG 7A); hTFIIA α/β , a full-length 1.1 kb EcoRI-EcoRI fragment from lambda11 or a 282 bp HaeIII-Hae III fragment from region II; hTFIIA γ , a full-length 355 bp NdeI-BamHI fragment or a 262 bp NdeI-EcoRI fragment from pRSEThp12; and actin controls (Clontech). DNA fragments were typically labeled with [α 32P]-dCTP using Ready-to-Go DNA Labeling Beads (Pharmacia) and purified over NICK columns (Pharmacia). Northern blots are hybridized for 1 hour in ExpressHyb solution (Clontech) and washed at 68° C for 1 hour. Membranes were typically exposed for 1-2 days to either XAR-5 film (Kodak) or a PhosphorImager screen (Molecular Dynamics). The results are shown in FIG 10A-10E.

Hybridization with a probe from the TFIIA α/β -like region of SALF reveals a 1.8 kb mRNA that is present in testis, but not in other tissues (FIG 10A, lane 12). The isolation of the ALF cDNA which corresponds to this species is illustrated in FIG 7B. The predicted 3.8 kb SALF mRNA is not visible in mRNA from any of the tissues examined, including placenta, liver, and testis from which SALF can be amplified by PCR (FIG 7A and C). These results indicate that ALF, and TFIIA α/β , are the major transcripts encoding human TFIIA large subunits, and that SALF is relatively rare. Hybridization with a probe specific for the 5'-end of SALF (5'-SALF) reveals a 6.5 kb species that is present at highest levels in heart, placenta, kidney, prostate, and uterus (FIG 10B, lanes 1, 3, 7, 11, and 13) and at lower levels in other tissues. This transcript, termed RNA6.5, was not detected using the ALF-specific probe (FIG 10A), indicating that it does not contain a downstream ALF domain. Thus, RNA6.5 is an independent human transcript that contains sequences similar, or identical, to those present at the 5'-end of SALF.

A dot blot purchased from Clontech containing 89-514 ng poly(A) mRNA from 50 adult and fetal tissues is hybridized as follows: [α 32P]-dCTP-labeled DNA is combined with 30 μ g Cot1 DNA (Boehringer-Mannheim) and 100 μ g salmon sperm DNA, denatured, and allowed to renature in 200 ml of 5X SSC at 68° C for 30 minutes prior to addition. After hybridization in 5 ml ExpressHyb solution at 65° C overnight with the probe, the blot was washed in 0.1X SSC at 55° C. Membranes were exposed as follows: FIG 11A, 19 hours; 11B, 2 hours 45 minutes; 11C, 14 hours; 11D, 25 hours, and 11E, 30 minutes. For

reprobing, Northern and dot blots were stripped twice with 0.5% SDS at 100° C, cooled to room temperature, and exposed overnight to confirm the loss of the previous signals. Quantitation of hybridization signals is performed using ImageQuaNT (Molecular Dynamics), and relative transcript levels in testis are determined by comparison to an average level from non-testis tissues. Ubiquitin (FIG 11E) is a control provided by the manufacturer (Clontech).

Using an ALF-specific probe, a strong signal was observed in testis that is due to the presence of the 1.8 kb ALF transcript (FIG 11A, position D1). In addition, weak signals were observed in approximately 24 of the remaining tissues, including small intestine, bladder, uterus, and prostate (positions E3, C5, C6, and C7). These signals indicate that ALF, or SALF, is expressed to low levels in non-testis tissues, and their detection in this study reflects the greater sensitivity of the dot blot. When this blot was stripped and reprobed with the 5'-SALF probe, signals were detected in all tissues (FIG 11B), with highest levels in placenta, uterus, spinal cord, and fetal kidney (positions F4, C6, B7, and G3) and several others, and lower levels in the remaining tissues. Because this probe detected high levels of RNA6.5 (but not SALF) in Northern analysis, the signals in Figure 6B are primarily due to the expression of RNA6.5.

Further inspection of the data reveals that the signals detected with the ALF- specific probe in FIG 11A are present in a range of tissues that is nearly identical to those observed in FIG 11B. This holds true for approximately 20 tissues, including bladder, uterus, prostate, ovary, placenta (positions C5, C6, C7, D2, and F4), and others, but not for testis (position D1). Likewise, the absence of signals in Figure 6A correlates with the absence of signals in FIG 11B. The results suggest a relationship between the expression of RNA6.5 with ALF-containing transcripts (possibly SALF) present at low levels in non-testis tissues. Hybridization with human TFIIA α/β - and TFIIA γ -specific probes (FIG 11C and 11D) shows that the corresponding mRNAs are expressed in all tissues. Quantitation of the results confirms that ALF (50-fold), TFIIA α/β (4-fold), and TFIIA γ (10-fold) are enriched in testis tissue.

EXAMPLE 4
PRODUCTION OF ALF AND SALF POLYPEPTIDES

To prepare recombinant ALF protein for functional assays, a 479 amino acid histidine-tagged polypeptide that spans residues Val7 to Trp478 was overexpressed and purified. Primers used in these studies had the corresponding sequences as follows: A1 (5'-ACTACTCATATGGCACACCACCATCACCATGTACCTAACTCTACAGATC T-3') (SEQ ID NO.: 14) and A2 (5'-AGTAGTGGATCCTTACCACTCTGCATCACC-3') (SEQ ID NO.: 15) were used to create a 1,445 bp NdeI-BamHI PCR fragment whose reading frame begins with the N-terminal extension MHHHHHHV (SEQ ID NO.: 16) and terminates with the natural TAA stop codon. This construct does not encode the first six amino acids (MACLNP, SEQ ID NO.: 17) found in the intact testis-derived ALF cDNA. After subcloning into pRSETC (Invitrogen), the resulting construct (pRSET-ALF) was transformed into *E. coli* BL21(DE3)pLysS (Novagen) and was expressed and purified essentially as follows. Cells were grown in LB media at 37° C to an OD₆₀₀ of ~0.5, and production of the 69 kD recombinant ALF protein is induced with 2 mM IPTG. Cells were harvested 3 hours post-induction, solubilized in Buffer A (0.1 M NaH₂PO₄, 0.01 M Tris pH 8.0, and either 6 M guanidine or 8 M urea), and sonicated five times for 30 seconds. The denatured cell lysate (~20 ml) was incubated with 2 ml Ni-NTA agarose resin (Qiagen) at room temperature for 1 hour. The resin was washed successively with Buffer A containing 8 M urea at pH 8.0, 6.3, and 5.9, and bound polypeptides are eluted at pH 3.5. Preparation of expression constructs for rat TFIIA α/β and rat TFIIA γ subunits (Genbank Accession numbers AF000943 and AF000944, respectively) and purification of the corresponding 55 and 12 kD recombinant proteins were performed. For transcription studies the recombinant p69 and p12 proteins were codialyzed in order to prevent precipitation of the p12 subunit.

The predicted size of this polypeptide is 53 kD, but the mobility on SDS-PAGE is 69 kD (FIG 12A, lane 2). This observation is similar to results showing that the predicted 42 kD product of hTFIIA α/β migrates at 55 kD (3,4), and may be due to the effect of charged region III. The mobilities of the purified recombinant rat TFIIA α/β (p55) and TFIIA γ (p12)

subunits used in these studies are also shown in FIG 12A (lanes 3 and 4). These polypeptides are at least 98% identical to their human counterparts.

A related procedure is used to prepare human TBP. Specifically, TBP was expressed in *E. coli* BL21(DE3)pLysS (Novagen) from a pET11d (Novagen) vector that contains a histidine tagged TBP open reading frame, induced with 2 mM IPTG at OD₆₀₀ 0.3 and purified at 4° C from the soluble fraction of the bacterial lysate over Ni-NTA agarose. Purification was performed by washing the resin with D700 buffer (20 mM HEPES, 20% glycerol, 0.2 mM EDTA, 10 mM β-mercaptoethanol, 0.5 mM PMSF, and 700 mM KCl) that contained 5 mM, 10 mM and 15 mM imidazole, and eluting bound polypeptides with D700 buffer that contained 100 mM imidazole. Recombinant proteins were dialyzed against Buffer C (10 mM Tris pH 7.9, 2 mM DTT, 20% glycerol, and 0.5 mM PMSF) containing 100 mM KCl prior to use.

To express SALF in a rabbit reticulocyte lysate system, primers NN1 (5'-TACTGCTCGAGCAACTTAGAGT-3') (SEQ ID NO.: 18) and 2a2-8 were used to generate a 2,988 bp product from pRACE4. An internal 2,207 bp XhoI-BglII fragment (aa 1-716) derived from this PCR product was then inserted into the XhoI-BglII digested pT7T3D vector that contains EST ID259637. Because an internal BglIII-BglII fragment that spans aa 717-1,084 was excised during preparation of this vector, this fragment was later reinserted in the appropriate orientation to create a full-length SALF ORF (pT7T3-SALF). This construct (0.8 mg) was used to program rabbit reticulocyte lysates in the presence of [³⁵S]-methionine as described by the manufacturer (Promega). Labeled polypeptides are separated on 8% SDS-PAGE gels, and visualized by autoradiography. To determine whether this full-length SALF cDNA construct is capable of directing the translation of an intact protein, *in vitro* transcription-translation reactions were performed.

As shown in FIG 12D, rabbit reticulocyte lysates programmed with pT7T3-SALF produced an [³⁵S]-methionine- labeled polypeptide that migrated at 170 kD (compared to a predicted size of 132 kD). Lysates programmed with pT7T3-SALF truncated at an internal EcoRI site at nucleotide position 960 produced a 36 kD product similar to the predicted size of 32 kD (data not shown). These results demonstrate that although SALF contains a

suboptimal ATG initiation codon (AAGATGT) and encodes a large ORF composed of two distinct regions, it can be translated efficiently.

EXAMPLE 5

5

ALF IS A TRANSCRIPTION FACTOR FOR RNA POLYMERASE II.

Functionality of ALF was demonstrated in TBP-dependent mobility shift assays and in RNA polymerase II-dependent in vitro transcription assays. Mobility shift assays were performed using 10 fmol of a [γ -³²P] ATP kinase-labeled TATA-containing an oligonucleotide that spans nucleotides -40 to -16 of the Adenovirus Major Late (AdML) promoter. Binding reactions (25 μ l final volume) were performed in 10 mM HEPES (pH 10 7.9), 2% (wt/vol) PEG-8000, 60 mM KCl, 5 mM DTT, 0.2 mM EDTA, 5 mM ammonium sulfate, 4 mM MgCl₂, and 8% glycerol. Recombinant rat p55 (30 ng; 29 nM), rat p12 (1.1 ug; 3.5 uM), human ALF (180 ng; 137 nM) and human TBP (125 ng; 133 nM) were added to reactions as indicated. Reactions were incubated for 30 minutes at room temperature, and complexes are separated on native 5% polyacrylamide gels containing 0.5X TBE and 5% 15 glycerol. Competition experiments contain either cold AdML TATA or SP1 oligonucleotides, and antibody supershift reactions contain 2-4 μ l of rabbit polyclonal antiserum raised against the 55 kD hTFIIA α/β polypeptide (3).

10

15

20

25

The activity of polypeptides was tested in electrophoretic mobility shift assays under conditions in which TATA-Binding Protein (TBP) alone is unable to bind DNA (FIG 12B, lane 1). The presence of TFIIA α/β (p55) and TFIIA γ (p12) stabilized the TBP-DNA interaction via TFIIA $\alpha/\beta/\gamma$ -TBP-DNA complex formation (lane 2). Likewise, the recombinant ALF (p69) polypeptide, in conjunction with the TFIIA γ (p12) subunit, was able to form ALF/ γ -TBP-DNA complexes (lane 5). Formation of this complex depends on the presence of both ALF and TFIIA γ . Although ALF (p69) is 102 amino acids longer than TFIIA α/β (p55) and migrates as a larger species in SDS-PAGE, the ALF/ γ -TBP- DNA complex migrates slightly faster than the TFIIA $\alpha/\beta/\gamma$ -TBP-DNA complex (lanes 2 and 5). These reactions are run side-by-side on the same gel using ALF and TFIIA subunits that have been purified and renatured using the same procedure. The specificity of ALF/ γ -TBP-DNA

complexes is similar to TFIIA α / β / γ -TBP-DNA complexes, as judged by competition with specific TATA (lanes 3 and 6) and nonspecific Sp1-site (lanes 4 and 7) oligonucleotides. In addition, both complexes are supershifted to the well when co-incubated with antiserum against hTFIIA α / β (lanes 8 and 9), indicating that ALF and TFIIA α / β are immunologically related, and are present in the respective complexes.

To demonstrate that ALF is a functional polypeptide that regulates gene expression, TFIIA-dependent *in vitro* transcription assays are performed. For this purpose, advantage was taken of the fact that TFIIA α / β contains an intrinsic seven-histidine region that allows for the efficient removal of TFIIA from HeLa cell nuclear extracts using Ni-NTA agarose. In brief, 200 μ l of extract were incubated with 100 μ l Ni-NTA agarose resin for 30 minutes at 4 °C in the presence of 400 mM KCl. Control extracts were processed similarly, except that no Ni-NTA agarose was present. After microcentrifugation for 5 minutes, the supernatants were removed and dialyzed for 3 hours against Buffer C that contains 100 mM KCl. Transcription reactions were performed using a template (pMLC2AT) that contains the AdML promoter upstream of a G-free cassette. The template was linearized at a SmaI site just beyond the G-free cassette prior to use. Each reaction (20 μ l) contained: 8 μ l nuclear extract (~60 μ g protein), 2 μ l (550 ng) of recombinant p69 (0.22 μ M) and p12 (0.9 μ M) proteins, 1 μ g pMLC2AT, 10 mM HEPES (pH 7.5), 25 mM KCl, 6 mM MgCl₂, 625 μ M UTP, 625 μ M ATP, 35 μ M CTP, 200 μ M O-methyl-GTP, 3% glycerol, 0.7 μ l [α -32P] CTP and 37.3 units of RNAGuard (Pharmacia). After incubation at 30° C for 45 minutes, the reactions were terminated by adding 270 μ l stop solution (0.25 M NaCl, 1% SDS, 20 mM Tris pH 7.5, 5 mM EDTA and 66.7 μ g/ml tRNA) and extracted with an equal volume of 1:1 phenol/chloroform. Ethanol precipitated transcripts were resuspended in formamide-containing loading dye and electrophoresed on 5% acrylamide gels containing 1X TBE and 8 M urea. Depleted extracts were transcriptionally inactive, but were restored to normal activity by the addition of TFIIA. As shown in FIG 12C (lane 1), control (undepleted) extracts produce a [γ ³²P]-CTP labeled G-free RNA transcript were expressed under the control of the AdML promoter (pMLC2AT). The addition of recombinant ALF (p69) and TFIIA γ (p12) to these extracts did not enhance transcription (lane 2).

TFIIA-depleted extracts were transcriptionally inactive, and were not affected by the re-addition of either ALF (p69) or TFIIA γ (p12) alone (lanes 3-5). The addition of both ALF (p69) and TFIIA γ (p12), however, restored transcription to the level observed with control extracts (lane 6). The results of the electrophoretic mobility shift and in vitro transcription assays shown in FIG 12B and 12C, demonstrate that ALF has TFIIA α/β -like functional activity via TBP, and that both ALF and TFIIA α/β require TFIIA γ , or a functionally similar subunit, for activity.

While this invention has been described in reference to illustrative embodiments, this description is not intended to be construed in a limiting sense. Various modifications and combinations of the illustrative embodiments, as well as other embodiments of the invention, will be apparent to persons skilled in the art upon reference to the description. It is therefore intended that the appended claims encompass any such modifications or embodiments.

SEQUENCE LISTING

5 <110> DeJong Dr., Jeff

10 <120> Transcription Factors Related to TFIIA

<130> 119941-1053

15

<140>

<141>

20

<160> 20

25

<170> PatentIn Ver. 2.0

30

<210> 1

<211> 1617

35

<212> DNA

<213> Homo sapiens

40

<220>

<221> CDS

<222> (16)..(1449)

5

<400> 1

gctggagggtg ctgtc atg gcc tgc ctc aac ccg gtg cct aaa ctc tac aga 51

Met Ala Cys Leu Asn Pro Val Pro Lys Leu Tyr Arg

10

1 5 10

15

tct gta att gaa gat gta att gaa gga gtt cgg aat cta ttt gct gaa 99

Ser Val Ile Glu Asp Val Ile Glu Gly Val Arg Asn Leu Phe Ala Glu

20

15 20 25

gaa ggt ata gag gaa caa gtt tta aaa gac ttg aag cag ctc tgg gaa 147

25

Glu Gly Ile Glu Glu Gln Val Leu Lys Asp Leu Lys Gln Leu Trp Glu

30 35 40

30

acc aag gtt ttg cag tct aaa gca aca gaa gac ttc ttc aga aat agc 195

Thr Lys Val Leu Gln Ser Lys Ala Thr Glu Asp Phe Phe Arg Asn Ser

35

45 50 55 60

atc caa tca cct ctg ttt act ctt cag ttg ccg cac agc ttg cac caa 243

40

Ile Gln Ser Pro Leu Phe Thr Leu Gln Leu Pro His Ser Leu His Gln

65 70 75

aca ttg caa tcg tca aca gca tca tta gtt att cct gct ggt aga act 291

5 Thr Leu Gln Ser Ser Thr Ala Ser Leu Val Ile Pro Ala Gly Arg Thr

80 85 90

10

ctt cca agt ttt acc aca gca gaa ctg ggc act tca aac tcc agt gca 339

Leu Pro Ser Phe Thr Thr Ala Glu Leu Gly Thr Ser Asn Ser Ser Ala

15

95 100 105

20 aac ttt act ttt cct ggt tat ccc att cat gta cca gca ggt gtg aca 387
20 Asn Phe Thr Phe Pro Gly Tyr Pro Ile His Val Pro Ala Gly Val Thr

110 115 120

25

cta cag act gta tct ggt cac ctt tat aaa gtc aat gta cca att atg 435

Leu Gln Thr Val Ser Gly His Leu Tyr Lys Val Asn Val Pro Ile Met

30

125 130 135 140

35

gtg aca gag act tct gga aga gca ggt att ctt cag cat cca att cag 483

Val Thr Glu Thr Ser Gly Arg Ala Gly Ile Leu Gln His Pro Ile Gln

145 150 155

40

caa gta ttt caa cag ctt ggc cag cct tca gta ata caa act agt gtt 531

*

Gln Val Phe Gln Gln Leu Gly Gln Pro Ser Val Ile Gln Thr Ser Val

160 165

170

5

cca caa ttg aat cca tgg tct ctt caa gca act act gaa aaa tca cag 579

Pro Gln Leu Asn Pro Trp Ser Leu Gln Ala Thr Thr Glu Lys Ser Gln
10

175 180 185

15 aga att gaa acc gtg cta cag caa ccc gca att cta cct tct ggg cca 627

Arg Ile Glu Thr Val Leu Gln Gln Pro Ala Ile Leu Pro Ser Gly Pro

190 195 200

20

gta gat agg aaa cac tta gaa aat gcc acc agt gat ata ctt gta tct 675

25 Val Asp Arg Lys His Leu Glu Asn Ala Thr Ser Asp Ile Leu Val Ser

205 210 215 220

30

cct gga aat gag cat aaa atc gtg cct gaa gct ttg ttg tgt cat cag 723

Pro Gly Asn Glu His Lys Ile Val Pro Glu Ala Leu Leu Cys His Gln

35

225 230 235

40

gaa agt tct cac tat atc agt ctt cca ggt gtt gta ttt tct cca cag 771

Glu Ser Ser His Tyr Ile Ser Leu Pro Gly Val Val Phe Ser Pro Gln

240 245 250

gtc tct caa aca aat tct gat gtg gag tca gtg ctc agt ggt tca gct 819

5 Val Ser Gln Thr Asn Ser Asp Val Glu Ser Val Leu Ser Gly Ser Ala

255

260

265

10

agc atg gct caa aat ctg cat gat gag tcc ctc tcc aca agc cct cat 867

Ser Met Ala Gln Asn Leu His Asp Glu Ser Leu Ser Thr Ser Pro His

15

270

275

280

20

ggg gct ctc cac cag cac gtg act gat att cag ctt cat att ctt aaa 915

Gly Ala Leu His Gln His Val Thr Asp Ile Gln Leu His Ile Leu Lys

285

290

295

300

25

aat agg atg tat gga tgt gat tct gta aag caa cca aga aat ata gag 963

Asn Arg Met Tyr Gly Cys Asp Ser Val Lys Gln Pro Arg Asn Ile Glu

30

305

310

315

35

gaa ccc agc aac ata cct gta tca gag aag gat tct aat tct cag gtg 1011

Glu Pro Ser Asn Ile Pro Val Ser Glu Lys Asp Ser Asn Ser Gln Val

320

325

330

40

gat tta agc att cgg gtt act gat gat att ggt gaa ata att caa 1059

Asp Leu Ser Ile Arg Val Thr Asp Asp Asp Ile Gly Glu Ile Ile Gln

335

340

345

5

gta gat gga agc ggt gat aca tct.tcc aat gaa gaa ata gga agt aca 1107

10 Val Asp Gly Ser Gly Asp Thr Ser Ser Asn Glu Glu Ile Gly Ser Thr
350 355 360

15 aga gat gca gat gag aat gaa ttt cta ggg aat att gac ggg gga gat 1155

Arg Asp Ala Asp Glu Asn Glu Phe Leu Gly Asn Ile Asp Gly Gly Asp

365 370 375 380

20

ctg aag gta cct gaa gaa gaa gct gac agt att tca aat gag gat tca 1203

25 Leu Lys Val Pro Glu Glu Ala Asp Ser Ile Ser Asn Glu Asp Ser
385 390 395

30

gcc aca aac agt agt gat aat gaa gac cct caa gta aac att gta gaa 1251

Ala Thr Asn Ser Ser Asp Asn Glu Asp Pro Gln Val Asn Ile Val Glu

35 400 405 410

40 40 40 40 gag gac cct tta aat tct gga gat gat gtt agt gaa cag gat gtg cca 1299

Glu Asp Pro Leu Asn Ser Gly Asp Asp Val Ser Glu Gln Asp Val Pro

415 420 425

gac ctg ttt gac acg gat aat gta att gtc tgt cag tat gat aag att 1347

5 Asp Leu Phe Asp Thr Asp Asn Val Ile Val Cys Gln Tyr Asp Lys Ile

430

435

440

10

cat cga agc aag aac aaa tgg aaa ttc tat ttg aaa gat ggt gtt atg 1395

His Arg Ser Lys Asn Lys Trp Lys Phe Tyr Leu Lys Asp Gly Val Met

15

445 450 455 460

20

tgt ttt gga ggg aga gac tat gta ttt gca aaa gcc att ggt gat gca 1443

Cys Phe Gly Gly Arg Asp Tyr Val Phe Ala Lys Ala Ile Gly Asp Ala

465

470

475

25

gag tgg taaaccttgt gagctcagta catctatttt gtgaacatca gttggactat 1499

Glu Trp

30

atgcataatt gtgaattcat ttttattttt aatatagtcc agcacagagc tgttcaaatt 1559

35

ttagttcac tgtatggaat ttaataaaat tataattcag atgcagatac aattacac 1617

40

<210> 2

<211> 478

<212> PRT

5

<213> Homo sapiens

<400> 2

10

Met Ala Cys Leu Asn Pro Val Pro Lys Leu Tyr Arg Ser Val Ile Glu

1

5

10

15

15

Asp Val Ile Glu Gly Val Arg Asn Leu Phe Ala Glu Glu Gly Ile Glu

20

25

30

20

Glu Gln Val Leu Lys Asp Leu Lys Gln Leu Trp Glu Thr Lys Val Leu

25

35

40

45

30

Gln Ser Lys Ala Thr Glu Asp Phe Phe Arg Asn Ser Ile Gln Ser Pro

50

55

60

35

Leu Phe Thr Leu Gln Leu Pro His Ser Leu His Gln Thr Leu Gln Ser

65

70

75

80

40

Ser Thr Ala Ser Leu Val Ile Pro Ala Gly Arg Thr Leu Pro Ser Phe

85

90

95

60

Thr Thr Ala Glu Leu Gly Thr Ser Asn Ser Ser Ala Asn Phe Thr Phe

5

100

105

110

Pro Gly Tyr Pro Ile His Val Pro Ala Gly Val Thr Leu Gln Thr Val

10

115

120

125

15

Ser Gly His Leu Tyr Lys Val Asn Val Pro Ile Met Val Thr Glu Thr

130

135

140

20

Ser Gly Arg Ala Gly Ile Leu Gln His Pro Ile Gln Gln Val Phe Gln

145

150

155

160

25

Gln Leu Gly Gln Pro Ser Val Ile Gln Thr Ser Val Pro Gln Leu Asn

165

170

175

30

Pro Trp Ser Leu Gln Ala Thr Thr Glu Lys Ser Gln Arg Ile Glu Thr

35

180

185

190

40

Val Leu Gln Gln Pro Ala Ile Leu Pro Ser Gly Pro Val Asp Arg Lys

195

200

205

His Leu Glu Asn Ala Thr Ser Asp Ile Leu Val Ser Pro Gly Asn Glu

210

215

220

5

His Lys Ile Val Pro Glu Ala Leu Leu Cys His Gln Glu Ser Ser His

225

230

235

240

10

Tyr Ile Ser Leu Pro Gly Val Val Phe Ser Pro Gln Val Ser Gln Thr

15

245

250

255

Asn Ser Asp Val Glu Ser Val Leu Ser Gly Ser Ala Ser Met Ala Gln

20

260

265

270

25

Asn Leu His Asp Glu Ser Leu Ser Thr Ser Pro His Gly Ala Leu His

275

280

285

30

Gln His Val Thr Asp Ile Gln Leu His Ile Leu Lys Asn Arg Met Tyr

290

295

300

35

Gly Cys Asp Ser Val Lys Gln Pro Arg Asn Ile Glu Glu Pro Ser Asn

305

310

315

320

40

Ile Pro Val Ser Glu Lys Asp Ser Asn Ser Gln Val Asp Leu Ser Ile

325 330 335

5 Arg Val Thr Asp Asp Asp Ile Gly Glu Ile Ile Gln Val Asp Gly Ser

340 345 350

10 Gly Asp Thr Ser Ser Asn Glu Glu Ile Gly Ser Thr Arg Asp Ala Asp

355 360 365

15 Glu Asn Glu Phe Leu Gly Asn Ile Asp Gly Gly Asp Leu Lys Val Pro

370 375 380

20

Glu Glu Glu Ala Asp Ser Ile Ser Asn Glu Asp Ser Ala Thr Asn Ser

25 385 390 395 400

30 Ser Asp Asn Glu Asp Pro Gln Val Asn Ile Val Glu Glu Asp Pro Leu
405 410 415

35 Asn Ser Gly Asp Asp Val Ser Glu Gln Asp Val Pro Asp Leu Phe Asp
420 425 430

40 Thr Asp Asn Val Ile Val Cys Gln Tyr Asp Lys Ile His Arg Ser Lys
435 440 445

Asn Lys Trp Lys Phe Tyr Leu Lys Asp Gly Val Met Cys Phe Gly Gly

5 450 455 460

Arg Asp Tyr Val Phe Ala Lys Ala Ile Gly Asp Ala Glu Trp

10 465 470 475

15

<210> 3

<211> 3824

20 <212> DNA

<213> Homo sapiens

25

<220>

<221> CDS

30 <222> (115)..(3660)

35 <400> 3

ggactttggg actggacaga cctggtcaca gtctaggttc tacatcttac tggtcgagca 60

40 acttttagagt caaccttattt gatttcttga caagaccaca atctgatccc aaag atg 117

Met

5 tgc tcc aca aat cca ggc aaa tgg gtc acc ttt gat gat gat cct gct 165
Cys Ser Thr Asn Pro Gly Lys Trp Val Thr Phe Asp Asp Asp Pro Ala

10 5 10 15

gtt caa tct tct caa aag tca aag aat ttt cct ctg gag aat caa ggt 213
15 Val Gln Ser Ser Gln Lys Ser Lys Asn Phe Pro Leu Glu Asn Gln Gly

 20 25 30

20 gtc tgt aga cca aat gga ctg aag ctg aac cct cct ggc ctc agg gaa 261
Val Cys Arg Pro Asn Gly Leu Lys Leu Asn Pro Pro Gly Leu Arg Glu

25 35 40 45

30 ttt ccc agt gga tct tcc tcc acc agc agc act cct ctc tcc tcc ccc 309
Phe Pro Ser Gly Ser Ser Thr Ser Ser Thr Pro Leu Ser Ser Pro

 50 55 60 65

35 att gta gat ttt tat ttc agt cca gga cct cca agt aac tct cct ctt 357
Ile Val Asp Phe Tyr Phe Ser Pro Gly Pro Pro Ser Asn Ser Pro Leu

40 70 75 80

tct aca cct acc aaa gac ttc cca ggt ttt cct ggc atc ccc aaa gca 405

Ser Thr Pro Thr Lys Asp Phe Pro Gly Phe Pro Gly Ile Pro Lys Ala

5

85

90

95

10 ggg act cat gtg ctt tat cct att cca gaa tca tct tca gac agc cca 453

Gly Thr His Val Leu Tyr Pro Ile Pro Glu Ser Ser Ser Asp Ser Pro

100

105

110

15

ctc gca ata tca gga gga gaa tct tcc tta ctg cct acc aga cca aca 501

Leu Ala Ile Ser Gly Gly Glu Ser Ser Leu Leu Pro Thr Arg Pro Thr

20

115

120

125

25

tgt tta tcc cat gcc ttg tta ccc agt gac cac tca tgt aca cat cca 549

Cys Leu Ser His Ala Leu Leu Pro Ser Asp His Ser Cys Thr His Pro

130

135

140

145

30

act ccc aaa gta ggt ctt cca gat gaa gtt aat cct caa cag gct gaa 597

35

Thr Pro Lys Val Gly Leu Pro Asp Glu Val Asn Pro Gln Gln Ala Glu

150

155

160

40

agc cta gga ttc caa agt gat gat ctc ccc cag ttt cag tat ttt cga 645

Ser Leu Gly Phe Gln Ser Asp Asp Leu Pro Gln Phe Gln Tyr Phe Arg

165

170

175

5 gag gac tgt gct ttt tca agt cca ttt cgg aaa gat gaa ggc agt gat 693

Glu Asp Cys Ala Phe Ser Ser Pro Phe Arg Lys Asp Glu Gly Ser Asp

180

185

190

10

tcc cat ttc acc ctt gac cca cca gga agc aaa aag atg ttc tca tca 741

15 Ser His Phe Thr Leu Asp Pro Pro Gly Ser Lys Lys Met Phe Ser Ser

195

200

205

20

aga aac aag gag atg cct att gac caa aaa agc cta aat aag tgt tca 789

Arg Asn Lys Glu Met Pro Ile Asp Gln Lys Ser Leu Asn Lys Cys Ser

25

210 215 220 225

30

ctc aac tat atc tgt gag aag ctt gaa cat ctc cag tca gct gag aac 837

Leu Asn Tyr Ile Cys Glu Lys Leu Glu His Leu Gln Ser Ala Glu Asn

230

235

240

35

caa gac tca ctt aga agt ttg tct atg cac tgt cta tgt gct gaa gaa 885

Gln Asp Ser Leu Arg Ser Leu Ser Met His Cys Leu Cys Ala Glu Glu

40

245

250

255

aat gcc tct tcc ttt gtc ccc cac aca ctc ttc agg agt cag cca aaa 933

Asn Ala Ser Ser Phe Val Pro His Thr Leu Phe Arg Ser Gln Pro Lys

5

260

265

270

10

tcc gga tgg tct ttc atg ctg aga att cct gag aag aag aat atg atg 981

Ser Gly Trp Ser Phe Met Leu Arg Ile Pro Glu Lys Lys Asn Met Met

275

280

285

15

tct tcc cgg caa tgg gga cca att ttt ctg aaa gtt ttg cct gga gga 1029

Ser Ser Arg Gln Trp Gly Pro Ile Phe Leu Lys Val Leu Pro Gly Gly

20

290 295 300 305

25

att ttg cag atg tat tat gaa cag gga tta gaa aaa cca ttt aaa gag 1077

Ile Leu Gln Met Tyr Tyr Glu Gln Gly Leu Glu Lys Pro Phe Lys Glu

310

315

320

30

ata cag ctt gat cca tat tgt agg ctt tct gaa ccc aag gtt gag aac 1125

Ile Gln Leu Asp Pro Tyr Cys Arg Leu Ser Glu Pro Lys Val Glu Asn

325

330

335

40

ttc agt gta gca gga aaa atc cac act gtg aag att gaa cat gtg tct 1173

Phe Ser Val Ala Gly Lys Ile His Thr Val Lys Ile Glu His Val Ser

340 345 350

5 tac aca gaa aaa agg aaa tac cat tct aag aca gaa gta gtt cat gaa 1221
Tyr Thr Glu Lys Arg Lys Tyr His Ser Lys Thr Glu Val Val His Glu

355 360 365

10

cct gac ata gag cag atg ctg aag ttg ggg tcc aca tcg tac cat gac 1269
Pro Asp Ile Glu Gln Met Leu Lys Leu Gly Ser Thr Ser Tyr His Asp

370 375 380 385

20

ttc ctt gac ttt ctg act act gtg gag gag gag ctg atg aag ttg cca 1317
Phe Leu Asp Phe Leu Thr Thr Val Glu Glu Glu Leu Met Lys Leu Pro

390 395 400

25

30

gct gtt tca aaa cca aaa aag aac tac gag gag caa gaa att tcc ttg 1365
Ala Val Ser Lys Pro Lys Lys Asn Tyr Glu Glu Gln Glu Ile Ser Leu

405 410 415

35

gaa att gtg gac aac ttt tgg ggt aaa gtc aca aaa gaa gga aaa ttt 1413
Glu Ile Val Asp Asn Phe Trp Gly Lys Val Thr Lys Glu Gly Lys Phe

420 425 430

40

gtt gaa agt gct gtg ata act caa att tat tgc ctc tgc ttt gtg aat 1461

Val Glu Ser Ala Val Ile Thr Gln Ile Tyr Cys Leu Cys Phe Val Asn

5 435 440 445

10 ggg aac ctg gaa tgc ttt tta acc ttg aat gac ctt gag ttg ccg aag 1509

Gly Asn Leu Glu Cys Phe Leu Thr Leu Asn Asp Leu Glu Leu Pro Lys

15 450 455 460 465

cga gat gaa tcc tat tat gag aag gac tca gaa aaa aag ggg att gat 1557

Arg Asp Glu Ser Tyr Tyr Glu Lys Asp Ser Glu Lys Lys Gly Ile Asp

20 470 475 480

25 att ctt gac tac cat ttt cat aag tgt gtg aat gta caa gaa ttt gag 1605

Ile Leu Asp Tyr His Phe His Lys Cys Val Asn Val Gln Glu Phe Glu

30 485 490 495

caa tca aga atc att aag ttt gta cct ctg gat gcc tgc cgg ttt gag 1653

35 Gln Ser Arg Ile Ile Lys Phe Val Pro Leu Asp Ala Cys Arg Phe Glu

500 505 510

40 ctg atg cgt ttc aag act ttg tat aat ggg gat aat ctt ccc ttt tcc 1701

Leu Met Arg Phe Lys Thr Leu Tyr Asn Gly Asp Asn Leu Pro Phe Ser

515

520

525

5 ttg aag tct gta gtg gtt gtc cag gga gca tac gtg gaa ctt cag gct 1749

Leu Lys Ser Val Val Val Val Gln Gly Ala Tyr Val Glu Leu Gln Ala

530

535

540

545

10

ttt gtc aac atg gcc tca ttg gcg cag agg tca tcc tat gct ggt tcc 1797

15 Phe Val Asn Met Ala Ser Leu Ala Gln Arg Ser Ser Tyr Ala Gly Ser

550

555

560

20

tta agg tcc tgt gac aat ata agg ata cac ttt cct gtc cca tcg cag 1845

Leu Arg Ser Cys Asp Asn Ile Arg Ile His Phe Pro Val Pro Ser Gln

25

565

570

575

30

tgg atc aag gcc ctt tgg acc atg aac ctc cag agg cag aag tct ctg 1893

Trp Ile Lys Ala Leu Trp Thr Met Asn Leu Gln Arg Gln Lys Ser Leu

580

585

590

35

aaa gct aaa atg aac cgc cga gca tgt ctg ggg agt tta cag gaa ctt 1941

Lys Ala Lys Met Asn Arg Arg Ala Cys Leu Gly Ser Leu Gln Glu Leu

40

595

600

605

gaa tct gaa cct gtc att caa gtc act gtg ggg tca gca aaa tat gag 1989

Glu Ser Glu Pro Val Ile Gln Val Thr Val Gly Ser Ala Lys Tyr Glu

5 610 615 620 625

10 agt gcc tac cag gca gtg gta tgg aag ata gat cgg ctt cca gac aaa 2037

Ser Ala Tyr Gln Ala Val Val Trp Lys Ile Asp Arg Leu Pro Asp Lys

630 635 640

15

aat tca agt cta gat cat ccc cat tgt ctg tca tac aaa tta gag ctt 2085

Asn Ser Ser Leu Asp His Pro His Cys Leu Ser Tyr Lys Leu Glu Leu

20

645 650 655

25

gga tca gac caa gaa att ccc tct gat tgg tat cca ttt gct act gtt 2133

Gly Ser Asp Gln Glu Ile Pro Ser Asp Trp Tyr Pro Phe Ala Thr Val

30

660 665 670

cag ttt tcc gtg cct gac acc tgt gcc tca agg aca gag gtc agg tct 2181

35

Gln Phe Ser Val Pro Asp Thr Cys Ala Ser Arg Thr Glu Val Arg Ser

675 680 685

40

ctg gga gtg gag agt gat gtc cag cca cag aaa cat gtt cag cag cga 2229

Leu Gly Val Glu Ser Asp Val Gln Pro Gln Lys His Val Gln Gln Arg

	690	695	700	705		
5	gct tgc tac aac atc cag cct aaa ctc tac aga tct gta att gaa gat				2277	
	Ala Cys Tyr Asn Ile Gln Pro Lys Leu Tyr Arg Ser Val Ile Glu Asp					
10	710	715	720			
	gta att gaa gga gtt cg ^g aat cta ttt gct gaa gaa ggt ata gag gaa				2325	
15	Val Ile Glu Gly Val Arg Asn Leu Phe Ala Glu Glu Gly Ile Glu Glu					
	725	730	735			
20						
	caa gtt tta aaa gac ttg aag cag ctc tgg gaa acc aag gtt ttg cag				2373	
	Gln Val Leu Lys Asp Leu Lys Gln Leu Trp Glu Thr Lys Val Leu Gln					
25	740	745	750			
30	tct aaa gca aca gaa gac ttc ttc aga aat agc atc caa tca cct ctg					2421
	Ser Lys Ala Thr Glu Asp Phe Phe Arg Asn Ser Ile Gln Ser Pro Leu					
	755	760	765			
35						
	ttt act ctt cag ttg ccg cac agc ttg cac caa aca ttg caa tcg tca				2469	
	Phe Thr Leu Gln Leu Pro His Ser Leu His Gln Thr Leu Gln Ser Ser					
40	770	775	780	785		

aca gca tca tta gtt att cct gct ggt aga act ctt cca agt ttt acc 2517

Thr Ala Ser Leu Val Ile Pro Ala Gly Arg Thr Leu Pro Ser Phe Thr

5 790 795 800

aca gca gaa ctg ggc act tca aac tcc agt gca aac ttt act ttt cct 2565

10 Thr Ala Glu Leu Gly Thr Ser Asn Ser Ser Ala Asn Phe Thr Phe Pro

805 810 815

15

ggt tat ccc att cat gta cca gca ggt gtg aca cta cag act gta tct 2613

Gly Tyr Pro Ile His Val Pro Ala Gly Val Thr Leu Gln Thr Val Ser

20 820 825 830

25 ggt cac ctt tat aaa gtc aat gta cca att atg gtg aca gag act tct 2661

Gly His Leu Tyr Lys Val Asn Val Pro Ile Met Val Thr Glu Thr Ser

835 840 845

30

gga aga gca ggt att ctt cag cat cca att cag caa gta ttt caa cag 2709

35 Gly Arg Ala Gly Ile Leu Gln His Pro Ile Gln Gln Val Phe Gln Gln

850 855 860 865

40

ctt ggc cag cct tca gta ata caa act agt gtt cca caa ttg aat cca 2757

Leu Gly Gln Pro Ser Val Ile Gln Thr Ser Val Pro Gln Leu Asn Pro

870 875 880

5 tgg tct ctt caa gca act act gaa aaa tca cag aga att gaa acc gtg 2805

Trp Ser Leu Gln Ala Thr Thr Glu Lys Ser Gln Arg Ile Glu Thr Val

885 890 895

10

cta cag caa ccc gca att cta cct tct ggg cca gta gat agg aaa cac 2853

15 Leu Gln Gln Pro Ala Ile Leu Pro Ser Gly Pro Val Asp Arg Lys His

900 905 910

20

tta gaa aat gcc acc agt gat ata ctt gta tct cct gga aat gag cat 2901

Leu Glu Asn Ala Thr Ser Asp Ile Leu Val Ser Pro Gly Asn Glu His

25

915 920 925

30 aaa atc gtg cct gaa gct ttg ttg tgt cat cag gaa agt tct cac tat 2949

Lys Ile Val Pro Glu Ala Leu Leu Cys His Gln Glu Ser Ser His Tyr

930 935 940 945

35

atc agt ctt cca ggt gtt gta ttt tct cca cag gtc tct caa aca aat 2997

Ile Ser Leu Pro Gly Val Val Phe Ser Pro Gln Val Ser Gln Thr Asn

40

950 955 960

tct gat gtg gag tca gtg ctc agt ggt tca gct agc atg gct caa aat 3045

Ser Asp Val Glu Ser Val Leu Ser Gly Ser Ala Ser Met Ala Gln Asn

5 965 970 975

ctg cat gat gag tcc ctc tcc aca agc cct cat ggg gct ctc cac cag 3093

10 Leu His Asp Glu Ser Leu Ser Thr Ser Pro His Gly Ala Leu His Gln

980 985 990

15

cac gtg act gat att cag ctt cat att ctt aaa aat agg atg tat gga 3141

His Val Thr Asp Ile Gln Leu His Ile Leu Lys Asn Arg Met Tyr Gly

20

995 1000 1005

25 tgt gat tct gta aag caa cca aga aat ata gag gaa ccc agc aac ata 3189

Cys Asp Ser Val Lys Gln Pro Arg Asn Ile Glu Glu Pro Ser Asn Ile

1010 1015 1020 1025

30

cct gta tca gag aag gat tct aat tct cag gtg gat tta agc att cgg 3237

35 Pro Val Ser Glu Lys Asp Ser Asn Ser Gln Val Asp Leu Ser Ile Arg

1030 1035 1040

40

gtt act gat gat gat att ggt gaa ata att caa gta gat gga agc ggt 3285

Val Thr Asp Asp Asp Ile Gly Glu Ile Ile Gln Val Asp Gly Ser Gly

1045 1050 1055

5 gat aca tct tcc aat gaa gaa ata gga agt aca aga gat gca gat gag 3333

Asp Thr Ser Ser Asn Glu Glu Ile Gly Ser Thr Arg Asp Ala Asp Glu

1060 1065 1070

10

aat gaa ttt cta ggg aat att gac ggg gga gat ctg aag gta cct gaa 3381

15 Asn Glu Phe Leu Gly Asn Ile Asp Gly Gly Asp Leu Lys Val Pro Glu

1075 1080 1085

20

gaa gaa gct gac agt att tca aat gag gat tca gcc aca aac agt agt 3429

Glu Glu Ala Asp Ser Ile Ser Asn Glu Asp Ser Ala Thr Asn Ser Ser

25 1090 1095 1100 1105

30 gat aat gaa gac cct caa gta aac att gta gaa gag gac cct tta aat 3477

Asp Asn Glu Asp Pro Gln Val Asn Ile Val Glu Glu Asp Pro Leu Asn

1110 1115 1120

35

tct gga gat gat gtt agt gaa cag gat gtg cca gac ctg ttt gac acg 3525

Ser Gly Asp Asp Val Ser Glu Gln Asp Val Pro Asp Leu Phe Asp Thr

40 1125 1130 1135

gat aat gta att gtc tgt cag tat gat aag att cat cga agc aag aac 3573

Asp Asn Val Ile Val Cys Gln Tyr Asp Lys Ile His Arg Ser Lys Asn

5 1140 1145 1150

aaa tgg aaa ttc tat ttg aaa gat ggt gtt atg tgt ttt gga ggg aga 3621

10 Lys Trp Lys Phe Tyr Leu Lys Asp Gly Val Met Cys Phe Gly Gly Arg

1155 1160 1165

15

gac tat gta ttt gca aaa gcc att ggt gat gca gag tgg taaaccttgt 3670

Asp Tyr Val Phe Ala Lys Ala Ile Gly Asp Ala Glu Trp

20 1170 1175 1180

25 gagctcagta catctatttt gtgaacatca gttggactat attgcatatt gtgaattcat 3730

ttttatTTTg aatatAGTCC agcacAGAGC tGTTCAAATT ttTAGTTCAC tGTATGGAAT 3790

30

ttaataaaat tataattcag atgcagatac aatt 3824

35

<210> 4

40 <211> 1182

<212> PRT

<213> Homo sapiens

5

<400> 4

Met Cys Ser Thr Asn Pro Gly Lys Trp Val Thr Phe Asp Asp Asp Pro

10
10

5

10

15

Ala Val Gln' Ser Ser Gln Lys Ser Lys Asn Phe Pro Leu Glu Asn Gln

15

20

25

30

20

Gly Val Cys Arg Pro Asn Gly Leu Lys Leu Asn Pro Pro Gly Leu Arg

35

40

45

25

Glu Phe Pro Ser Gly Ser Ser Ser Thr Ser Ser Thr Pro Leu Ser Ser

50

55

60

30

Pro Ile Val Asp Phe Tyr Phe Ser Pro Gly Pro Pro Ser Asn Ser Pro

65

70

75

80

35

Leu Ser Thr Pro Thr Lys Asp Phe Pro Gly Phe Pro Gly Ile Pro Lys

85

90

95

40

Ala Gly Thr His Val Leu Tyr Pro Ile Pro Glu Ser Ser Ser Asp Ser

100 105 110

5 Pro Leu Ala Ile Ser Gly Gly Glu Ser Ser Leu Leu Pro Thr Arg Pro

115 120 125

10 Thr Cys Leu Ser His Ala Leu Leu Pro Ser Asp His Ser Cys Thr His

130 135 140

15

Pro Thr Pro Lys Val Gly Leu Pro Asp Glu Val Asn Pro Gln Gln Ala

145 150 155 160

20

Glu Ser Leu Gly Phe Gln Ser Asp Asp Leu Pro Gln Phe Gln Tyr Phe

25 165 170 175

30 Arg Glu Asp Cys Ala Phe Ser Ser Pro Phe Arg Lys Asp Glu Gly Ser

180 185 190

35 Asp Ser His Phe Thr Leu Asp Pro Pro Gly Ser Lys Lys Met Phe Ser

195 200 205

40

Ser Arg Asn Lys Glu Met Pro Ile Asp Gln Lys Ser Leu Asn Lys Cys

210 215 220

Ser Leu Asn Tyr Ile Cys Glu Lys Leu Glu His Leu Gln Ser Ala Glu

5 225 230 235 240

Asn Gln Asp Ser Leu Arg Ser Leu Ser Met His Cys Leu Cys Ala Glu

10 245 250 255

15 Glu Asn Ala Ser Ser Phe Val Pro His Thr Leu Phe Arg Ser Gln Pro

260 265 270

20 Lys Ser Gly Trp Ser Phe Met Leu Arg Ile Pro Glu Lys Lys Asn Met

275 280 285

25 Met Ser Ser Arg Gln Trp Gly Pro Ile Phe Leu Lys Val Leu Pro Gly

290 295 300

30

Gly Ile Leu Gln Met Tyr Tyr Glu Gln Gly Leu Glu Lys Pro Phe Lys

35 305 310 315 320

40 Glu Ile Gln Leu Asp Pro Tyr Cys Arg Leu Ser Glu Pro Lys Val Glu

325 330 335

Asn Phe Ser Val Ala Gly Lys Ile His Thr Val Lys Ile Glu His Val

340

345

350

5

Ser Tyr Thr Glu Lys Arg Lys Tyr His Ser Lys Thr Glu Val Val His

355

360

365

10

Glu Pro Asp Ile Glu Gln Met Leu Lys Leu Gly Ser Thr Ser Tyr His

15

370

375

380

20

Asp Phe Leu Asp Phe Leu Thr Thr Val Glu Glu Glu Leu Met Lys Leu

385

390

395

400

25

Pro Ala Val Ser Lys Pro Lys Lys Asn Tyr Glu Glu Gln Glu Ile Ser

405

410

415

30

Leu Glu Ile Val Asp Asn Phe Trp Gly Lys Val Thr Lys Glu Gly Lys

420

425

430

35

Phe Val Glu Ser Ala Val Ile Thr Gln Ile Tyr Cys Leu Cys Phe Val

435

440

445

40

Asn Gly Asn Leu Glu Cys Phe Leu Thr Leu Asn Asp Leu Glu Leu Pro

450

455

460

5 Lys Arg Asp Glu Ser Tyr Tyr Glu Lys Asp Ser Glu Lys Lys Gly Ile

465

470

475

480

10 Asp Ile Leu Asp Tyr His Phe His Lys Cys Val Asn Val Gln Glu Phe

485

490

495

15 Glu Gln Ser Arg Ile Ile Lys Phe Val Pro Leu Asp Ala Cys Arg Phe

500

505

510

20 Glu Leu Met Arg Phe Lys Thr Leu Tyr Asn Gly Asp Asn Leu Pro Phe

25 515 520 525
Ser Leu Lys Ser Val Val Val Val Gln Gly Ala Tyr Val Glu Leu Gln

30 530 535 540
Ala Phe Val Asn Met Ala Ser Leu Ala Gln Arg Ser Ser Tyr Ala Gly

35 545 550 555 560

40 Ser Leu Arg Ser Cys Asp Asn Ile Arg Ile His Phe Pro Val Pro Ser

565 570 575

Gln Trp Ile Lys Ala Leu Trp Thr Met Asn Leu Gln Arg Gln Lys Ser

5 580 585 590

Leu Lys Ala Lys Met Asn Arg Arg Ala Cys Leu Gly Ser Leu Gln Glu

10 595 600 605

15 Leu Glu Ser Glu Pro Val Ile Gln Val Thr Val Gly Ser Ala Lys Tyr

610 615 620

20 Glu Ser Ala Tyr Gln Ala Val Val Trp Lys Ile Asp Arg Leu Pro Asp

625 630 635 640

25 Lys Asn Ser Ser Leu Asp His Pro His Cys Leu Ser Tyr Lys Leu Glu

645 650 655

30

Leu Gly Ser Asp Gln Glu Ile Pro Ser Asp Trp Tyr Pro Phe Ala Thr

35 660 665 670

40 Val Gln Phe Ser Val Pro Asp Thr Cys Ala Ser Arg Thr Glu Val Arg

675 680 685

Ser Leu Gly Val Glu Ser Asp Val Gln Pro Gln Lys His Val Gln Gln

690

695

700

5

Arg Ala Cys Tyr Asn Ile Gln Pro Lys Leu Tyr Arg Ser Val Ile Glu

705

710

715

720

10

Asp Val Ile Glu Gly Val Arg Asn Leu Phe Ala Glu Glu Gly Ile Glu

15

725

730

735

20

Glu Gln Val Leu Lys Asp Leu Lys Gln Leu Trp Glu Thr Lys Val Leu

740

745

750

25

Gln Ser Lys Ala Thr Glu Asp Phe Phe Arg Asn Ser Ile Gln Ser Pro

755

760

765

30

Leu Phe Thr Leu Gln Leu Pro His Ser Leu His Gln Thr Leu Gln Ser

770

775

780

35

Ser Thr Ala Ser Leu Val Ile Pro Ala Gly Arg Thr Leu Pro Ser Phe

785

790

795

800

40

Thr Thr Ala Glu Leu Gly Thr Ser Asn Ser Ser Ala Asn Phe Thr Phe

805

810

815

5 Pro Gly Tyr Pro Ile His Val Pro Ala Gly Val Thr Leu Gln Thr Val

820

825

830

10 Ser Gly His Leu Tyr Lys Val Asn Val Pro Ile Met Val Thr Glu Thr

835

840

845

15 Ser Gly Arg Ala Gly Ile Leu Gln His Pro Ile Gln Gln Val Phe Gln

850

855

860

20 Gln Leu Gly Gln Pro Ser Val Ile Gln Thr Ser Val Pro Gln Leu Asn

25 Pro Trp Ser Leu Gln Ala Thr Thr Glu Lys Ser Gln Arg Ile Glu Thr

30 885 890 895

35 Val Leu Gln Gln Pro Ala Ile Leu Pro Ser Gly Pro Val Asp Arg Lys

900

905

910

40 His Leu Glu Asn Ala Thr Ser Asp Ile Leu Val Ser Pro Gly Asn Glu

915

920

925

" His Lys Ile Val Pro Glu Ala Leu Leu Cys His Gln Glu Ser Ser His

5 930 935 940

Tyr Ile Ser Leu Pro Gly Val Val Phe Ser Pro Gln Val Ser Gln Thr

10 945 950 955 960

15 Asn Ser Asp Val Glu Ser Val Leu Ser Gly Ser Ala Ser Met Ala Gln

965 970 975

20 Asn Leu His Asp Glu Ser Leu Ser Thr Ser Pro His Gly Ala Leu His

980 985 990

25 Gln His Val Thr Asp Ile Gln Leu His Ile Leu Lys Asn Arg Met Tyr

30 995 1000 1005

Gly Cys Asp Ser Val Lys Gln Pro Arg Asn Ile Glu Glu Pro Ser Asn

35 1010 1015 1020

40 Ile Pro Val Ser Glu Lys Asp Ser Asn Ser Gln Val Asp Leu Ser Ile
025 1030 1035 1040

Arg Val Thr Asp Asp Asp Ile Gly Glu Ile Ile Gln Val Asp Gly Ser

1045

1050

1055

5

Gly Asp Thr Ser Ser Asn Glu Glu Ile Gly Ser Thr Arg Asp Ala Asp

1060

1065

1070

10

Glu Asn Glu Phe Leu Gly Asn Ile Asp Gly Gly Asp Leu Lys Val Pro

15

1075

1080

1085

20

Glu Glu Glu Ala Asp Ser Ile Ser Asn Glu Asp Ser Ala Thr Asn Ser

1090

1095

1100

25

Ser Asp Asn Glu Asp Pro Gln Val Asn Ile Val Glu Glu Asp Pro Leu

105

1110

1115

1120

30

Asn Ser Gly Asp Asp Val Ser Glu Gln Asp Val Pro Asp Leu Phe Asp

1125

1130

1135

35

Thr Asp Asn Val Ile Val Cys Gln Tyr Asp Lys Ile His Arg Ser Lys

1140

1145

1150

40

Asn Lys Trp Lys Phe Tyr Leu Lys Asp Gly Val Met Cys Phe Gly Gly

1155

1160

1165

5 Arg Asp Tyr Val Phe Ala Lys Ala Ile Gly Asp Ala Glu Trp

1170

1175

1180

10

<210> 5

15 <211> 261

<212> DNA

<213> Homo sapiens

20

<220>

25 <221> CDS

<222> (1)..(30)

<223> Variable 3' end for both ALF and SALF

30

<400> 5

35 gca ttc cca aga agg aca tcg ttt aac acc taaactcatt taacaaagga 50

Ala Phe Pro Arg Arg Thr Ser Phe Asn Thr

1

5

10

40

tccgagaaga acaggacacag tgtggaaaga aatcttcttg tcatggcata ttgccttctt 110

atatttcttc tggaatcatg ttcgcttggc ttcctgatta aaaacacagt tttattgctc 170

5

tctgcactgc caaaccaata aatttacaga agagaaagct gtattccact gtaccccttg 230

10

cagcatcaat aaaactgaca gccaaaaaaaa a

261

15

<210> 6

<211> 10

20

<212> PRT

<213> Homo sapiens

25

<400> 6

Ala Phe Pro Arg Arg Thr Ser Phe Asn Thr

30

1

5

10

35

<210> 7

<211> 18

40

<212> DNA

<213> Homo sapiens

<400> 7

5 agaaattccc tctgattg

18

10

<210> 8

<211> 18

15

<212> DNA

<213> Homo sapiens

20

<400> 8

agtaacccga atgcttaa

18

25

<210> 9

30

<211> 18

<212> DNA

35

<213> Homo sapiens

<400> 9

40

atgctagctg aaccactg

18

<210> 10

5 <211> 27

<212> DNA

<213> Homo sapiens

10

<400> 10

15 ccatccta at acgactcact ataggc

27

20

<210> 11

<211> 23

25 <212> DNA

<213> Homo sapiens

30

<400> 11

actcactata gggctcgagc ggc

23

35

<210> 12

40 <211> 30

<212> DNA

<213> Homo sapiens

5 <400> 12

ccagaaggta gaattgcggg ttgctgttagc 30

10

<210> 13

15 <211> 28

<212> DNA

<213> Homo sapiens

20

<400> 13

25 ggtgctgtca tggcctgcct caacccgg 28

30

<210> 14

<211> 52

35 <212> DNA

<213> Homo sapiens

40

<400> 14

actactcata tggcacacca tcaccatcac catgtaccta aactctacag at 52

5 <210> 15

<211> 30

<212> DNA

10 <213> Homo sapiens

15 <400> 15

agtagtggat ccttaccact ctgcattcacc

30.

20

<210> 16

25 <211> 8

<212> PRT

<213> Homo sapiens

30

<400> 16

35 Met His His His His His Val

1

5

40

<210> 17

<211> 6

<212> PRT

5 <213> Homo sapiens

<400> 17

10 Met Ala Cys Leu Asn Pro

1

5

15

<210> 18

20 <211> 23

<212> DNA

25 <213> Homo sapiens

<400> 18

30 tactgctcga gcaacttttag agt

23

35

<210> 19

<211> 6

40 <212> PRT

<213> Homo sapiens

<400> 19

5 Ala Cys Leu Asn Pro Val

1 5

10

<210> 20

15 <211> 29

<212> DNA

<213> Homo sapiens

20

<400> 20

25 ggagtttcaa gtgcccgagg ctgctgtgg 29

30

References

1. Roeder, R.G. (1991) *Trends Biochem. Sci.* 21, 327-335.
2. Orphanides, G., Lagrange, T., and Reinberg, D. (1996) *Genes Dev.* 10, 2657-2683.
3. DeJong, J. and Roeder, R.G. (1993) *Genes Dev.* 7, 2220-2234.
4. Ma, D., Watanabe, H., Mermelstein, F., Admon, A., Oguri, K., Sun, X., Wada, T., Imai, T., Shiroya, T., Reinberg, D., and Handa, H. (1993) *Genes Dev.* 7, 2246-2257.
5. Ozer, J., Moore, P.A., Bolden, A.H., Lee, A., Rosen, C.A., and Leiberman, P. (1994) *Genes Dev.* 8, 2324-2335.
- 10 6. Sun, X., Ma, D., Sheldon, M., Yeung, K., and Reinberg, D. (1994) *Genes Dev.* 8, 2336-2348.
7. DeJong, J., Bernstein, R., and Roeder, R.G. (1995) *Proc. Natl. Acad. Sci.* 92, 3313-3317.
- 15 8. Ranish, J.A., Lane, W.S., and Hahn, S. (1992) *Science* 255, 1127-1129.
9. Yokomori, K., Admon, A., Goodrich, J.A., Chen, J.-L., and Tjian, R. (1993) *Genes Dev.* 7, 2235-2245.
- 10 10. Yokomori, K., Zeidler, M.P., Chen, J.-L., Verrijzer, C.P., and Tjian, R. (1994) *Genes Dev.* 8, 2313-2323.
11. Bernstein, R., DeJong, J., and Roeder, R.G. (1994) *J. Biol. Chem.* 269, 24361-24366.
- 20 12. Tan, S., Hunziker, Y., Sargent, D.F., and Richmond, T.J. (1996) *Nature* 381, 127-134.
13. Geiger, J.H., Hahn, S., Lee, S., and Sigler, P.B. (1996) *Science* 272, 830-836.
14. Buratowski, S., Hahn, S., Sharp, P.A., and Guarente, L. (1989) *Cell* 56, 549-561.
- 25 15. Lee, D.K., DeJong, J., Hashimoto, S., Horikoshi, M., and Roeder, R.G. (1992) *Mol. Cell. Biol.* 12, 5189-5196.
16. Imbalzano, A.N., Zaret, K.S., and Kingston, R.E. (1994) *J. Biol. Chem.* 269, 8280-8286.
- 30 17. Weidman, C.A., Netter, R.C., Benjamin, L.R., McAllister, J.J., Schmiedekamp, L.A., Coleman, R.A., and Pugh, B.F. (1997) *J. Mol. Biol.* 271, 61-75.
18. Meisterernst, M. and Roeder, R.G. (1991) *Cell* 67, 557-567.
19. Inostroza, J.A., Mermelstein, F.H., Ha, I., Lane, W.S., and Reinberg, D. (1992) *Cell* 70, 477-489.
- 35 20. Merino, A., Madden, K.R., Lane, W., Champoux, J.J., and Reinberg, D. (1993) *Nature* 365, 227-232.
21. Ge, H. and Roeder, R.G. (1994) *J. Biol. Chem.* 269, 17136-17140.
22. Kirov, N.C., Lieberman, P.M., and Rushlow, C. (1996) *EMBO J.* 15, 7079-7087.
23. Auble, D.T. and Hahn, S. (1993) *Genes Dev.* 7, 844-856.
- 40 24. Auble, D.T., Hansen, K.E., Mueller, C.G., Lane, W.S., Thorner, J., and Hahn, S. (1994) *Genes Dev.* 8, 1920-1934.
25. Chicca, J.J. II, Auble, D.T., and Pugh, B.F. (1998) *Mol. Cell. Biol.* 18, 1701-1710.

26. Kokubo, T., Swanson, M.J., Nishikawa, J.I., Hinnebusch, A.G., and Nakatani, Y. (1998) *Mol. Cell. Biol.* 18, 1003-1012.
27. Ozer, J., Mitsouras, K., Zerby, D., Carey, M., and Lieberman, P.M. (1998) *J. Biol. Chem.* 273, 14293-14300.
- 5 28. Wang, W., Gralla, J.D., and Carey, M. (1992) *Genes Dev.* 6, 1716-1727.
29. Lieberman, P.M. and Berk, A.J. (1994) *Genes Dev.* 8, 995-1006.
30. Ma, D., Olave, I., Merino, A., and Reinberg, D. (1996) *Proc. Natl. Acad. Sci.* 93, 6583-6588.
- 10 31. Ozer, J., Bolden, A.H., and Lieberman, P.M. (1996) *J. Biol. Chem.* 271, 11182-11190.
32. Ge, H. and Roeder, R.G. (1994) *Cell* 78, 513-523.
33. Shykind, B.M., Kim, J., and Sharp, P.A. (1995) *Genes Dev.* 9, 1354-1365.
- 15 34. Oelgeschlager, T., Chiang, C.-M., and Roeder, R.G. (1996) *Nature* 382, 735-738.
35. Chi, T. and Carey, M. (1996) *Genes Dev.* 10, 2540-2550.
36. Emami, K.H., Jain, A., and Smale, S.T. (1997) *Genes Dev.* 11, 3007-3019.
- 20 37. Lennon, C.G., Auffray, C., Polymeropoulos, M., and Soares, M.B. (1996) *Genomics* 33, 151-152.
38. Kozak, M. (1984) *Nuc. Acids Res.* 12, 857-872.
39. Andrews, J., Smith, M., Merakovsky, J., Coulson, M., Hannan, F., and Kelly, L.E. (1996) *Genetics* 143, 1699-1711.
- 25 40. Wilson et al. (1994) *Nature* 368, 32-38.
41. Grigliatti, T.A., Hall, L., Rosenbluth, R., and Suzuki, D.T. (1973) *Mol. Gen. Genet.* 120, 107-114.
42. Thurieau, C., Brosius, J., Burne, C., Jolles, P., Keen, J.H., Mattalia, R.J., Chow, E.P., Ramachandran, K.L., and Kirchhausen, T. (1988) *DNA* 7, 663-669.
43. Nakayama, Y., Goebl, M., O'Brine Greco, B., Lemmon, S., Chow, E.P.-C., and Kirchhausen, T. (1991) *Eur. J. Bioch.* 202, 569-574.
44. Keen, J.H. (1990) *Ann. Rev. Bioch.* 59, 415-438.
45. Hirst, J. and Robinson, M.S. (1998) *Bioch. Biophys. Acta* 1404, 173-193.

30

What is claimed is:

1. An isolated polynucleotide sequence comprising a nucleotide sequence that encodes a polypeptide of SEQ ID NO. 2, or fragments of said sequence.

5

2. A composition comprising a polypeptide sequence set out in SEQ ID NO. 2 and fragments thereof, or those which are functionally equivalent.

10

3. The DNA segment of claim 1, that encodes the human testis-specific transcriptional factor ALF.

4. The DNA segment of claim 1, comprising a human testis-specific transcriptional factor that includes at least 30 contiguous nucleotides from position 16 to 1617 of SEQ ID NO.:1.

15

5. The DNA segment of claim 1, comprising a human testis-specific transcriptional factor that encodes the amino acids of SEQ ID NO.: 2.

20

6. The DNA segment of claim 1, whereby the segment encodes amino acids 1 to 478 of SEQ ID NO.: 2.

25

7. The DNA segment of claim 1, positioned under the control of a promoter.

8. The DNA segment of claim 1, further defined as comprising a recombinant vector.

9. An isolated nucleic acid segment characterized as:
- (a) a nucleic acid segment comprising a sequence that consists essentially of at least 30 contiguous nucleotides that have substantially the same sequence as, or are complementary to, 30 contiguous nucleic acids of SEQ ID NO.:1; or
 - 5 (b) a nucleic acid segment of from 14 to about 1434 nucleotides in length that hybridize to the nucleic acid segment of SEQ ID NO.:1, or complement thereof, under high stringency hybridization conditions.

10. The nucleic acid segment of claim 9, wherein the segment comprises a sequence region of at least 30 contiguous nucleotides from SEQ ID NO.:1, or the complement thereof.

15. The nucleic acid segment of claim 9, wherein the segment comprises a sequence region of at least about 30 nucleotides; or wherein the segment is about 30 nucleotides in length.

12. The nucleic acid segment of claim 11, wherein the segment comprises a sequence region of at least about 30 nucleotides; or wherein the segment is about 30 nucleotides in length.

20. The nucleic acid segment of claim 12, wherein the segment comprises a sequence region of at least about 50 nucleotides; or wherein the segment is about 50 nucleotides in length.

25. The nucleic acid segment of claim 13, wherein the segment comprises a sequence region of at least about 100 nucleotides; or wherein the segment is about 100 nucleotides in length.

15. The nucleic acid segment of claim 14, wherein the segment comprises a sequence region of at least about 200 nucleotides; or wherein the segment is about 200 nucleotides in length.

5 16. The nucleic acid segment of claim 15, wherein the segment comprises a sequence region of at least about 500 nucleotides; or wherein the segment is about 500 nucleotides in length.

10 17. The nucleic acid segment of claim 16, wherein the segment comprises a sequence region of at least about 1000 nucleotides; or wherein the segment is about 1000 nucleotides in length.

15 18. The nucleic acid segment of claim 16, wherein the segment comprises a sequence region of about 1434 nucleotides; or wherein the segment is about 1434 nucleotides in length.

19. The nucleic acid segment of claim 9, wherein the segment is up to 10,000 base pairs in length.

20 20. The nucleic acid segment of claim 19, wherein the segment is up to 5,000 base pairs in length.

21. The nucleic acid segment of claim 20, wherein the segment is up to 3,000 base pairs in length.

25 22. The nucleic acid segment of claim 21, wherein the segment is up to 1,000 base pairs in length.

23. The nucleic acid segment of claim 9, further defined as a DNA segment.

24. The nucleic acid segment of claim 9, further defined as a RNA segment.

25. A recombinant host cell comprising a DNA segment as defined in claim 9.

5

26. The recombinant host cell of claim 25, wherein the DNA segment is introduced into the cell by means of a recombinant vector.

10 27. The recombinant host cell of claim 25, wherein the whole cell expresses the DNA segment to produce the encoded human testis-specific transcriptional factor protein or peptide wherein said protein or peptide has the amino acid sequence of SEQ ID NO.:2.

28. The recombinant host cell of claim 25, further defined as a bacterial host cell.

15 29. The recombinant host cell of claim 28, wherein the bacterial host cell is E. coli.

30. A method of using a DNA segment that includes an isolated testis-specific transcriptional factor gene, comprising the steps of:

- (a) preparing a recombinant vector in which a testis-specific transcriptional factor gene encoding DNA segment, or a fragment thereof, is positioned under the control of a promoter wherein said testis-specific transcriptional factor gene has the sequence of SEQ ID NO.:2;
- (b) introducing said recombinant vector into recombinant host cell;
- (c) culturing a recombinant host cell under conditions effective to allow expression of the encoded testis-specific transcriptional factor gene protein or peptide; and
- (d) collecting said testis-specific transcriptional factor gene protein or peptide.

31. A method of making a recombinant vector comprising inserting the isolated DNA segment of SEQ ID NO.:1 into a vector.

32. An isolated DNA segment comprising the sequence of Genbank Accession number AF106857, its complement, and fragments of said sequence.

33. An isolated polypeptide comprising a mature polypeptide having an amino acid sequence encoded by a nucleic acid segment that is at least 95% identical to SEQ ID NO.:1.

34. The isolated polypeptide of claim 33, comprising amino acids 1 to 478 of SEQ ID NO.: 2.

35. An isolated polynucleotide sequence comprising a nucleotide sequence that encodes a polypeptide of SEQ ID NO. 4, or fragments of said sequence.

36. The isolated polynucleotide sequence of claim 35, comprising a nucleic acid molecule that comprises the nucleotide sequence of SEQ ID NO. 3, or fragments of said sequence.

5 37. The DNA segment of claim 35, that encodes a human transcriptional factor related to the *Drosophila* Stoned gene.

38. The DNA segment of claim 35, that encodes the human transcriptional factor SALF.

10 39. The DNA segment of claim 35, comprising a human testis-specific transcriptional factor that includes at least 30 contiguous nucleotides from position 16 to 3824 of SEQ ID NO.:3.

15 40. The DNA segment of claim 35, comprising a human testis-specific transcriptional factor that encodes the amino acids of SEQ ID NO.: 4.

41. The DNA segment of claim 35, which encodes amino acids 1 to 11821 of SEQ ID NO.: 4.

20 42. The DNA segment of claim 35, positioned under the control of a promoter.

43. The DNA segment of claim 35, further defined as comprising a recombinant vector.

25 44. An isolated nucleic acid segment characterized as:

(a) a nucleic acid segment comprising a sequence that consists essentially of at least 30 contiguous nucleotides that have substantially the same sequence as, or are complementary to, 30 contiguous nucleic acids of SEQ ID NO.:3; or

(b) a nucleic acid segment of from 14 to about 3824 nucleotides in length that hybridize to the nucleic acid segment of SEQ ID NO.:3, or complement thereof, under high stringency hybridization conditions.

5 45. The nucleic acid segment of claim 43, wherein the segment comprises a sequence region of at least 30 contiguous nucleotides from SEQ ID NO.:3, or the complement thereof.

10 46. The nucleic acid segment of claim 43, wherein the segment comprises a sequence region of at least about 30 nucleotides; or wherein the segment is about 30 nucleotides in length.

15 47. The nucleic acid segment of claim 45, wherein the segment comprises a sequence region of at least about 30 nucleotides; or wherein the segment is about 30 nucleotides in length.

20 48. The nucleic acid segment of claim 46, wherein the segment comprises a sequence region of at least about 50 nucleotides; or wherein the segment is about 50 nucleotides in length.

49. The nucleic acid segment of claim 47, wherein the segment comprises a sequence region of at least about 100 nucleotides; or wherein the segment is about 100 nucleotides in length.

25 50. The nucleic acid segment of claim 48, wherein the segment comprises a sequence region of at least about 200 nucleotides; or wherein the segment is about 200 nucleotides in length.

51. The nucleic acid segment of claim 49, wherein the segment comprises a sequence region of at least about 500 nucleotides; or wherein the segment is about 500 nucleotides in length.

5 52. The nucleic acid segment of claim 50, wherein the segment comprises a sequence region of at least about 1000 nucleotides; or wherein the segment is about 1000 nucleotides in length.

10 53. The nucleic acid segment of claim 51, wherein the segment comprises a sequence region of about 3824 nucleotides; or wherein the segment is about 3824 nucleotides in length.

15 54. The nucleic acid segment of claim 43, wherein the segment is up to 10,000 base pairs in length.

55. The nucleic acid segment of claim 53, wherein the segment is up to 5,000 base pairs in length.

20 56. The nucleic acid segment of claim 54, wherein the segment is up to 3,000 base pairs in length.

57. The nucleic acid segment of claim 55, wherein the segment is up to 1,000 base pairs in length.

25 58. The nucleic acid segment of claim 43, further defined as a DNA segment.

59. The nucleic acid segment of claim 43, further defined as a RNA segment.

60. A recombinant host cell comprising a DNA segment as defined in claim 43.

51. The recombinant host cell of claim 59, wherein the DNA segment is introduced into the cell by means of a recombinant vector.

5 62. The recombinant host cell of claim 59, wherein the whole cell expresses the DNA segment to produce the encoded transcriptional factor protein or peptide wherein said protein or peptide has the amino acid sequence of SEQ ID NO.:4.

10 63. The recombinant host cell of claim 59, further defined as a bacterial host cell.

15 64. The recombinant host cell of claim 62, wherein the bacterial host cell is E. coli.

15. A method of using a DNA segment that includes an isolated testis-specific transcriptional factor gene, comprising the steps of:

- 20 (a) preparing a recombinant vector in which a human transcriptional factor gene encoding DNA segment is positioned under the control of a promoter wherein said testis-specific transcriptional factor gene has the sequence of SEQ ID NO.:4;
- 25 (b) introducing said recombinant vector into recombinant host cell;
- (c) culturing a recombinant host cell under conditions effective to allow expression of the encoded transcriptional factor gene protein or peptide; and
- (d) collecting the human testis-specific transcriptional factor gene protein or peptide.

25 66. A method of making a recombinant vector comprising inserting the isolated DNA segment of SEQ ID NO.:3 into a vector.

67. An isolated DNA segment comprising the sequence of Genbank Accession number AF026169, its complement, and fragments of said sequence.

5 68. An isolated polypeptide comprising a mature polypeptide having an amino acid sequence encoded by a nucleic acid segment that is at least 95% identical to SEQ ID NO.:3.

10 69. The isolated polypeptide of claim 20, comprising amino acids 1 to 1182 of SEQ ID NO.: 4.

15 70. An isolated nucleic acid segment characterized as:

- (a) a nucleic acid segment comprising a sequence that consists essentially of at least 30 contiguous nucleotides that have substantially the same sequence as, or are complementary to, 30 contiguous nucleic acids of SEQ ID NO.:5; or
- (b) a nucleic acid segment of from 1 to about 30 nucleotides in length that hybridize to the nucleic acid segment of SEQ ID NO.:5, or complement thereof, under high stringency hybridization conditions.

TRANSCRIPTION FACTORS RELATED TO TFIIA

ABSTRACT OF THE DISCLOSURE

The invention provides human polynucleotide sequences that encode transcription factor polypeptides that are termed ALF and SALF, and an alternative C-terminal sequence:
5 The invention includes ALF, SALF and alternative C-terminus polypeptides, peptides, fusion proteins, expression vectors, agonists, antagonists, host cells that overexpress these polypeptides, including transgenic animals, and recombinant knock-out animals that cannot express the relevant RNAs and polypeptides. The invention also provides methods for the detection, diagnosis, screening, and monitoring disorders related to inappropriate expression,
10 production, or activity of ALF and SALF, and provides methods to increase or decrease gene expression with respect to treating disorders related to inappropriate or ineffectual patterns of gene expression.

15

691850.4